



# ***STIC Search Report***

## ***Biotech-Chem Library***

**STIC Database Tracking Number: 190167**

**TO: Manjunath N Rao**  
**Location: rem/2A01/2C70**  
**Art Unit: 1652**  
**Friday, May 19, 2006**  
**Case Serial Number: 09/211691**

**From: Barb O'Bryen**  
**Location: Biotech-Chem Library**  
**Remsen 1a69**  
**Phone: 571-272-2518**

*BOB*  
**barbara.obryen@uspto.gov**

### **Search Notes**

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77025

190167

mry

**STIC-Biotech/ChemLib**

**From:** Chan, Christina  
**Sent:** Tuesday, May 16, 2006 1:53 PM  
**To:** Rao, Manjunath N.; STIC-Biotech/ChemLib  
**Subject:** RE: RUSH sequence search request for 09/211691

Please ~~rush~~ Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
MAY 16 2006  
STIC/CHEN, Christina  
(STIC)

-----Original Message-----

**From:** Rao, Manjunath N.  
**Sent:** Tuesday, May 16, 2006 1:50 PM  
**To:** Chan, Christina  
**Subject:** RUSH sequence search request for 09/211691

Hello Christina,

Please authorize the request below as RUSH. The reason being, this is an RCE and applicants have now included the following sequences in their claims.

Many Thanks  
-Manjunath

**Manjunath N. Rao**  
Art Unit 1652, Room 2A01,  
Mail Box in Room 2C70,  
Remsen Building, USPTO  
400, Dulany St.  
Alexandria, VA.  
Phone: 571-272-0939

-----  
**From:** Manjunath N. Rao  
Art Unit 1652, Room 2A01  
Mail Box in Room 2C70  
Phone: 272-0939

**Date:** 5-16-06

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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Please search the following as soon as possible for application with serial number  
**09/211691**

1. SEQ ID NO: 5 and 6 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results

If you have any questions please call me at the above phone number.

Thanks

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 00:44:40 ; Search time 789.333 Seconds

(without alignments)  
2997.535 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37

Sequence: 1 gcacgaatctgcggctgaagaagctcttgcacc 37

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb\_pl:\*

5: gb\_pr:\*

6: gb\_ro:\*

7: gb\_sts:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vl:\*

11: gb\_ov:\*

12: gb\_hlg:\*

13: gb\_in:\*

14: gb\_cm:\*

15: gb\_da:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	26.4	71.4	2039	15 NMU60660	U60660 Neisseria m
2	26.4	71.4	110000	15 AE002098_09	Continuation (10 o
3	26.4	71.4	331801	15 NMA4Z2491	AL162755 Neisseria
4	26.4	71.4	349980	2 CS238429	CS238429 Sequence
5	26.4	71.4	349980	2 CS238430	CS238430 Sequence
6	26.4	71.4	349980	2 AX044030	AX044030 Sequence
7	26.4	71.4	349980	2 AX044031	AX044031 Sequence
8	26	70.3	1116	2 ARI05309	ARI05309 Sequence
9	26	70.3	1116	2 ARI44756	ARI44756 Sequence
10	26	70.3	1116	2 BD009732	BD009732 Sequence
11	26	70.3	1116	2 NMU60661	BD009732 Recombina
12	26	70.3	1116	15 NMU60662	U60661 Neisseria m
13	24.4	65.9	110000	15 NMU60663	U60662 Neisseria m
14	24.4	65.9	110000	4 AP008212_046	Continuation (47 o
15	24.4	65.9	110000	4 AP008210_235	Continuation (236
16	24.4	65.9	110000	4 AP008211_091	Continuation (92 o
17	24.4	65.9	110000	4 AP008211_092	Continuation (93 o
18	24.4	65.9	139298	4 GSJN00012	AL606441 Oryza sat

C 19	24.4	65.9	164925	4 AC121362	AC121362 Oryza sat
C 20	24.4	65.9	174500	4 AP004738	AP004738 Oryza sat
C 21	23.8	64.3	110000	12 CR828282_2	Continuation (3 of
C 22	23.8	64.3	179667	12 CR854852	CR854852 Danio rer
C 23	23.8	64.3	191778	12 CR856633	CR856633 Danio rer
C 24	23.8	64.3	197593	12 CR855360	CR855360 Danio rer
C 25	23.8	64.3	215198	6 AC113180	AC113180 Mus muscu
C 26	23.8	64.3	227326	12 CR854836	CR854836 Danio rer
C 27	23.8	64.3	231100	11 AL954312	AL954312 Zebrafish
C 28	23.8	64.3	256720	6 AC110241	AC110241 Mus muscu
C 29	23.6	63.8	726	2 BD149112	BD149112 Primer fo
C 30	23.6	63.8	726	2 AX869050	AX869050 Sequence
C 31	23.4	63.2	425	5 AY859405	AY859405 Macaca mu
C 32	23.4	63.2	80050	5 AC124833	AC124833 Homo sapi
C 33	23.4	63.2	178555	12 AC027397	AC027397 Homo sapi
C 34	23.2	62.7	2613	2 CQ598079	CQ598079 Sequence
C 35	23.2	62.7	5356	10 AB069671	AB069671 Crimaean-C
C 36	23.2	62.7	5356	10 AB069672	AB069672 Crimaean-C
C 37	23.2	62.7	5356	10 AY223476	AY223476 Crimaean-C
C 38	23.2	62.7	57335	12 AC015272	AC015272 Drosophila
C 39	23.2	62.7	188459	13 AC008312	AC008312 Drosophila
C 40	23.2	62.7	197597	13 AC011253	AC011253 Drosophila
C 41	23.2	62.7	315844	13 AE003671	AE003671 Drosophila
C 42	23	62.2	1359	2 CQ734837	CQ734837 Sequence
C 43	23	62.2	1734	2 AR578067	AR578067 Sequence
C 44	23	62.2	2161	5 BC032942	BC032942 Homo sapi
C 45	23	62.2	2228	2 BD158353	BD158353 Primer to

## ALIGNMENTS

RESULT 1	NMU60660	2039 bp	DNA	linear	BCI 08-NOV-1996
LOCUS	Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete cds, and isocitrate dehydrogenase and cytochrome c genes, partial				
DEFINITION	Neisseria meningitidis				
ACCESSION	U60660				
VERSION	U60660.1	GI:1546002			
KEYWORDS	Neisseria meningitidis				
SOURCE	Neisseria meningitidis				
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.				
REFERENCE	1 (bases 1 to 2039)				
AUTHORS	Gilbert M., Watson D.C., Cunningham A.M., Jennings M.P., Young N.M. and Wakarchuk W.W.				
TITLE	Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogen Neisseria meningitidis and Neisseria gonorrhoeae				
JOURNAL	J. Biol. Chem. 271 (45), 28271-28276 (1996)				
PUBMED	8910446				
REFERENCE	2 (bases 1 to 2039)				
AUTHORS	Gilbert M., Michniewicz J.J., Watson D.C. and Wakarchuk W.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-JUN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada				
FEATURES	Location/Qualifiers				
source	1..2039				
	/organism="Neisseria meningitidis"				
	/mol_type="genomic DNA"				
	/strain="MC58, NRC 4728"				
	/db_xref="taxon:487"				
	/note="lipooligosaccharide type: L3"				
	complement(1..140)				
	/note="similar to isocitrate dehydrogenase from Azotobacter vinelandii"				
	/codon_start=1				
	/transl_table=11				
	/product="isocitrate dehydrogenase"				
	/protein_id="AAC44540.1"				

CDS

/db\_xref="GI:1546003"  
 /translation="MTOKSTIVYHTDEAPALATQSLPIVQAFARHADIVTSDIS  
 LSG".1688  
 /note="Expression and functionality of the product were  
 both determined experimentally"  
 /codon\_start=1  
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 /protein\_id="AAC44541.1"  
 /db\_xref="GI:1546004"  
 /translation="MGKKAACIVLCIVCFPIPTFDRVNGCERNVSLKEKLFN  
 BEGPVILIRCYTTLQMKVABRIAQHPGSEFYVLMSENREKRYVFNQIKDAER  
 AYFPHLPYGLKSFNF1PTMAELKVKSMLEPKRYLASLEKVSIAAFISTYPAER  
 KTFDGTGNLIQSSSYIGDEFSVNGTIRKRFAMMIGDWSIAKTRNASDEHTIFKGL  
 KNIMDGRKRTYLPFDASELKTGDEGTGTRILIGSPDKEMKEISEKAANKFKIY  
 VAPHRQTJSGVTLNTPYVIEDYILREIKKNPHRYEITTFPGALITMKDFPNV  
 HVALKPAALPEDEWLEKPYALFTQSGIPILTFDDKN"  
 complement(1653..2039)  
 /note="similar to cytochrome c' from Rhodopseudomonas  
 gelatinosa"  
 /codon\_start=2  
 /transl\_table=11  
 /product="Cytochrome c'"  
 /protein\_id="AAC44542.1"  
 /db\_xref="GI:1546005"  
 /translation="RALPRAWSDGAFEAETKTPAAVAEKNAAAQTGLDEIKAYG  
 ETGASCSCSDSRAPR"

CDS

Query Match 71.4%; Score 26.4; DB 15; Length 2039;  
 Best Local Similarity 96.4%; Pred. No. 1.2;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAAAAGCCTTTGACC 37  
 |||||  
 Db 572 TATGGCCTTGAAAAAGCCTTTGACC 599

RESULT 2  
 AE002098\_09  
 WPCOMMENT

Sequence split into 23 fragments LOCUS AE002098 Accession AE002098

Fragment Name	Begin	End
AE002098_00	1	110000
AE002098_01	100001	210000
AE002098_02	200001	310000
AE002098_03	300001	410000
AE002098_04	400001	510000
AE002098_05	500001	610000
AE002098_06	600001	710000
AE002098_07	700001	810000
AE002098_08	800001	910000
AE002098_09	900001	1010000
AE002098_10	1000001	1110000
AE002098_11	1100001	1210000
AE002098_12	1200001	1310000
AE002098_13	1300001	1410000
AE002098_14	1400001	1510000
AE002098_15	1500001	1610000
AE002098_16	1600001	1710000
AE002098_17	1700001	1810000
AE002098_18	1800001	1910000
AE002098_19	1900001	2010000
AE002098_20	2000001	2110000
AE002098_21	2100001	2210000
AE002098_22	2200001	2272360

Continuation (10 of 23) of AE002098 from base 900001 (AE002098 Neisseria meningitidis MG

Query Match 71.4%; Score 26.4; DB 15; Length 110000;  
 Best Local Similarity 96.4%; Pred. No. 0.86;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAAAAGCCTTTGACC 37  
 |||||  
 Db 34787 TATGGCCTTGAAAAAGCCTTTGACC 34814

RESULT 3  
 NMA42491

LOCUS  
 DEFINITION  
 NMA42491  
 segment 4/7.  
 AL162755 AL157959  
 AL162755.2 GI:7379742

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 PARKHILL J., Achtmann M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Holt R.D., Jorgensen F., Devlin K., Felwell T., Hamlin N., Harty M., Jorgensen F., Leathem S., Mouton S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skellern J., Whitehead S., Spratt B.G. and Barrell B.G.  
 Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491  
 Nature 404 (6777), 502-506 (2000)  
 10761919

JOURNAL  
 PUBMED  
 10761919

REFERENCE  
 AUTHORS  
 PARKHILL J.  
 Direct Submission  
 Submitted (30-MAR-2000) Submitted on behalf of the Neisseria  
 sequencing team, Sanger Centre, Wellcome Trust Genome Campus,  
 Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENT  
 Notes:  
 Details of N. meningitidis sequencing at the Sanger Centre are  
 available on the World Wide Web.  
 (URL, [http://www.sanger.ac.uk/Projects/N\\_meningitidis/](http://www.sanger.ac.uk/Projects/N_meningitidis/)).  
 Location/Qualifiers  
 1..331801  
 /organism="Neisseria meningitidis Z2491"  
 /mol\_type="genomic DNA"  
 /strain="Z2491"  
 /db\_xref="taxon:122587"  
 /note="serogroup: A"  
 117..1333  
 /gene="NMA1040"  
 /pseudo  
 117..1333  
 /gene="NMA1040"  
 /note="NMA1040, possible type I restriction-modification  
 system specificity protein, pseudogene, len: 1217 bp;  
 N-terminus shows weak similarity to the C-terminal half of  
 TR:Q0359 (EMBL:L25415), hsdS18, Mycoplasma pulmonis  
 restriction-modification enzyme subunit S18 (336 aa)  
 fasta scores: E(): 2.3e-06, 26.2% identity in 141 aa  
 overlap and to many hypothetical restriction-modification  
 subunits. Also similar to NMA1041, fasta scores: E():  
 4.8e-10, 37.0% identity in 100 aa overlap. C-terminus  
 similar to part of SW:TI51.ECOLI (EMBL:X13145), hsdS,  
 Escherichia coli type I restriction enzyme Ecol1241  
 specificity protein (410 aa), fasta scores: E(): 1.9e-14,  
 39.6% identity in 182 aa overlap. Similar to NMA1040.E():  
 2.9e-09, 38.0% identity in 100 aa overlap. Contains Pfam  
 match to entry PF01420 Methylase\_S, Type I restriction  
 modification DNA specificity domain. Contains a G(8) tract  
 which would allow translation as an intact CDS, if  
 variable. Lies within a region of unusually low GC  
 content"  
 /pseudo  
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 /transl\_table=11  
 /product="pseudogene (putative type I





LOCUS	CS238429	349980 bp	DNA	linear	PAT 04-JAN-2006
DEFINITION	Sequence 111 from Patent EP1605061.				
ACCESSION	CS238429				
VERSION	CS238429.1	GI:84364856			
KEYWORDS					
SOURCE					
ORGANISM	Neisseria meningitidis				
REFERENCE	1. Neisseria meningitidis				
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
JOURNAL	Neisseriaceae; Neisseria.				
FEATURES					
source	1. Pizza, M. Patent: EP 1605061-A 111 14-DEC-2005; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US) Location/Qualifiers 1. .349980 /organism="Neisseria meningitidis" /mol_type="unassigned DNA" /db_xref="taxon:487" /note="Seq 1 to long, 2242716 replaced by new seq 1, from 1 to 349980 seq 110, from 300001 to 649980 seq 111, from 600001 to 949980 seq 112, from 900001 to 1249980 seq 113, from 1200001 to 1549980 seq 114, from 1500001 to 1849980 seq 115, from 1800001 to 2149980 seq 116, from 2100001 to 2242716"				
ORIGIN					
Query Match	71.4%; Score 26.4; DB 2; Length 349980;				
Best Local Similarity	96.4%; Pred. No. 0.78;				
Matches	27; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	10 TCTGGCTGAAAGCGCTGTTGACC 37				
DB	334750 TATGGCTTGAAAAAGCGCTGTTGACC 334777				
RESULT 5					
LOCUS	CS238430	349980 bp	DNA	linear	PAT 04-JAN-2006
DEFINITION	Sequence 112 from Patent EP1605061.				
ACCESSION	CS238430				
VERSION	CS238430.1	GI:84364857			
KEYWORDS					
SOURCE					
ORGANISM	Neisseria meningitidis				
REFERENCE	1. Neisseria meningitidis				
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
JOURNAL	Neisseriaceae; Neisseria.				
FEATURES					
source	1. Pizza, M. Patent: EP 1605061-A 112 14-DEC-2005; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US) Location/Qualifiers 1. .349980 /organism="Neisseria meningitidis" /mol_type="unassigned DNA" /db_xref="taxon:487" /note="Seq 1 to long, 2242716 replaced by new seq 1, from 1 to 349980 seq 110, from 300001 to 649980 seq 111, from 600001 to 949980 seq 112, from 900001 to 1249980 seq 113, from 1200001 to 1549980 seq 114, from 1500001 to 1849980 seq 115, from 1800001 to 2149980 seq 116, from 2100001 to 2242716"				
ORIGIN					
Query Match	71.4%; Score 26.4; DB 2; Length 349980;				
Best Local Similarity	96.4%; Pred. No. 0.78;				
Matches	27; Conservative	0; Mismatches	1; Indels	0; Gaps	0;

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QY      10 TCTGGGCTTGAAGGCTTGTGACC 37
        |||||||
Db      34750 TATGGCTTGAAGGCTTGTGACC 34777
        |||||||

RESULT 6
LOCUS   AX044030
DEFINITION Sequence 109 from Patent WO0066791.
ACCESSION AX044030
VERSION  AX044030.1  GI:11342914
KEYWORDS
SOURCE  .
ORGANISM Neisseria meningitidis
          Neisseria meningitidis
          Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
          Neisseriaceae; Neisseria.
REFERENCE
AUTHORS 1 Pizzo,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
          Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
          Scarlato,V., Rappunli,R., Fraxer,C.M. and Grandi,G.
          Neisseria genomic sequences and methods of their use
          Patent: WO 0066791-A 109 09-NOV-2000;
          CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
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              /db_xref="taxon:487"
              /note="sequence too long, cut in 8 pieces.
                seq 1: 1 to 349980 349980 bases
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                seq 109: 600001 to 949980 349980 bases
                seq 110: 900001 to 1249980 349980 bases
                seq 111: 1200001 to 1549980 349980 bases
                seq 112: 1500001 to 1849980 349980 bases
                seq 113: 1800001 to 2149980 349980 bases
                seq 114: 2100001 to 2272325 172325 bases"

ORIGIN
Query Match 71.4%; Score 26.4; DB 2; Length 349980;
Best Local Similarity 96.4%; Pred. No. 0.78;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 TCTGGGCTTGAAGGCTTGTGACC 37
        |||||||
Db      334749 TATGGCTTGAAGGCTTGTGACC 334776

RESULT 7
LOCUS   AX044031
DEFINITION Sequence 110 from Patent WO0066791.
ACCESSION AX044031
VERSION  AX044031.1  GI:11342915
KEYWORDS
SOURCE  .
ORGANISM Neisseria meningitidis
          Neisseria meningitidis
          Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
          Neisseriaceae; Neisseria.
REFERENCE
AUTHORS 1 Pizzo,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
          Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
          Scarlato,V., Rappunli,R., Fraxer,C.M. and Grandi,G.
          Neisseria genomic sequences and methods of their use
          Patent: WO 0066791-A 110 09-NOV-2000;
          CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
        source
          location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:487"
              /note="sequence too long, cut in 8 pieces.
                seq 1: 1 to 349980 349980 bases

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seq 108: 300001 to 649980 349980 bases  
seq 109: 600001 to 949980 349980 bases  
seq 110: 900001 to 124980 349980 bases  
seq 111: 120001 to 154980 349980 bases  
seq 112: 150001 to 184980 349980 bases  
seq 113: 180001 to 214980 349980 bases  
seq 114: 210001 to 2272325 172325 bases"

ORIGIN

Query Match 71.4%; Score 26.4; DB 2; Length 349980;  
Best Local Similarity 96.4%; Pred. No. 0.78;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCTGGGCTTGAAGGCTTGTGGACC 37  
Db 34749 TATGGCTTGAAGGCTTGTGGACC 34776

RESULT 8  
ARI05309  
LOCUS ARI05309 1116 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 1 from patent US 6096529.  
ACCESSION ARI05309  
VERSION ARI05309.1 GI:12818906  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1116)  
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.  
TITLE Recombinant alpha-2,3-sialyltransferases and their uses  
JOURNAL Patent: US 6096529-A 1 01-AUG-2000;  
FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTGTGGACC 37  
Db 2 TGGGCTTGAAGGCTTGTGGACC 27

RESULT 9  
ARI44756  
LOCUS ARI44756 1116 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6210933.  
ACCESSION ARI44756  
VERSION ARI44756.1 GI:15106623  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1116)  
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,N.Martin., Jennings,M.P. and  
Moxon,E.Richard.  
TITLE Recombinant alpha-2,3-sialyltransferases and their uses  
JOURNAL Patent: US 6210933-A 1 03-APR-2001;  
FEATURES  
source Location/Qualifiers  
1..1116  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTGTGGACC 37

Db 2 TGGGCTTGAAGGCTTGTGGACC 27

RESULT 10  
BD009732  
LOCUS BD009732 1116 bp DNA linear PAT 31-JAN-2002  
DEFINITION Recombinant alpha-2,3-sialyltransferases and their uses.  
ACCESSION BD009732  
VERSION BD009732.1 GI:18638105  
KEYWORDS JP 2001503961-A/1.  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE 1 (bases 1 to 1116)  
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.  
TITLE Recombinant alpha-2,3-sialyltransferases and their uses  
JOURNAL Patent: JP 2001503961-A 1 27-MAR-2001;  
COMMENT NATIONAL RESEARCH COUNCIL OF CANADA  
OS Neisseria meningitidis  
PN JP 2001503961-A/1  
PD 27-MAR-2001  
PF 10-JUN-1997 JP 1997526320  
PR MICHEL GILBERT,WARREN W WAKARCHUK,MARTIN N YOUNG, PI MICHAEL  
P JENNINGS  
PC C12N15/54,C12N15/70,C12N15/79,C12N9/10,C12N5/10,C12N1/21, PC  
C12P19/26  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT CDS 1..1116  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:487"

ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTGTGGACC 37  
Db 2 TGGGCTTGAAGGCTTGTGGACC 27

RESULT 11  
NMU60661  
LOCUS NMU60661 1116 bp DNA linear BCT 08-NOV-1996  
DEFINITION Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete  
cgs.  
ACCESSION U60661  
VERSION U60661.1 GI:1546006  
KEYWORDS  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE 1 (bases 1 to 1116)  
AUTHORS Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M.  
and Wakarchuk,W.W.  
TITLE Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from  
the bacterial pathogens Neisseria meningitidis and Neisseria  
gonorrhoeae  
JOURNAL J. Biol. Chem. 271 (45), 28271-28276 (1996)  
PUBMED 8910446  
REFERENCE 2 (bases 1 to 1116)  
AUTHORS Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUN-1996) Institute for Biological Sciences, National

Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada  
Location/Qualifiers

1. .1116  
/organism="Neisseria meningitidis"  
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/db\_xref="taxon:487"  
/note="Capsule type: Y; lipooligosaccharide type: L3"  
1. .1116  
/note="The gene product activity was determined experimentally"  
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KTFDDGTINLIQSSSYLGDEFVNGTIRKNNFRAMNIGDSIAKTRNASDEHYTIFRGL  
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## CDS

## ORIGIN

Query Match 70.3%; Score 26; DB 15; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TGGGCTTGAAAAAGCCTTGTGGACC 37  
|||||  
2 TGGGCTTGAAAAAGCCTTGTGGACC 27

## Db

RESULT 12  
NMU60662 1116 bp DNA linear BCT 13-DEC-1999  
LOCUS Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete  
DEFINITION cds.  
ACCESSION U60662 GI:6563405  
VERSION U60662.2  
KEYWORDS  
SOURCE  
ORGANISM  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 1116)  
Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M.  
and Wakarchuk,W.W.  
Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from  
the bacterial pathogens Neisseria meningitidis and Neisseria  
gonorrhoeae  
J. Biol. Chem. 271 (45), 28271-28276 (1996)  
8910446

JOURNAL  
PUBMED 2 (bases 1 to 1116)  
REFERENCE Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.  
AUTHORS Direct Submission  
TITLE Submitted (13-0UN-1996) Institute for Biological Sciences, National  
JOURNAL Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A  
0R6, Canada  
3 (bases 1 to 1116)  
REFERENCE Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.  
AUTHORS Direct Submission  
TITLE Submitted (13-DEC-1999) Institute for Biological Sciences, National  
JOURNAL Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A  
0R6, Canada

REMARK  
COMMENT Sequence update by submitter  
FEATURES On Dec 13, 1999 this sequence version replaced gi:1546008.  
1. .1116  
Location/Qualifiers  
/organism="Neisseria meningitidis"  
/mol\_type="genomic DNA"

## CDS

## ORIGIN

Query Match 70.3%; Score 26; DB 15; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TGGGCTTGAAAAAGCCTTGTGGACC 37  
|||||  
2 TGGGCTTGAAAAAGCCTTGTGGACC 27

## Db

RESULT 13  
NMU60663 1115 bp DNA linear BCT 08-NOV-1996  
LOCUS Neisseria meningitidis truncated alpha-2,3-sialyltransferase gene,  
DEFINITION complete cds.  
ACCESSION U60663 GI:1546010  
VERSION U60663.1  
KEYWORDS  
SOURCE  
ORGANISM  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
1 (bases 1 to 1115)  
Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M.  
and Wakarchuk,W.W.  
Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from  
the bacterial pathogens Neisseria meningitidis and Neisseria  
gonorrhoeae  
J. Biol. Chem. 271 (45), 28271-28276 (1996)  
8910446

JOURNAL  
PUBMED 2 (bases 1 to 1115)  
REFERENCE Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.  
AUTHORS Direct Submission  
TITLE Submitted (13-0UN-1996) Institute for Biological Sciences, National  
JOURNAL Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A  
0R6, Canada

FEATURES  
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Location/Qualifiers  
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/strain="M982B, NRCC 4725"  
/db\_xref="taxon:487"  
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1. .456  
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the alpha-2,3-sialyltransferase"  
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/db\_xref="GI:1546011"  
/translation="MSLKKACTVLCIVFCGIFYPFDNRVNHGERRNAVSLDKLFLN  
EEBEPVNLIFCYTILQMKVARIQAQHPGERFYVVLMSERNREKYDYFPQIKDKAER  
AYFFHLPGYGLNKSFNFIPTMAELKVKSMLEPKRYIYLALEKVSIAAFISTYPPAEI

## CDS

## ORIGIN

Query Match 65.9%; Score 24.4; DB 15; Length 1115;  
Best Local Similarity 96.2%; Pred. No. 10;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 12 TGGGCTGAAAAGCTGTTGACC 37  
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Db 2 TGAGCTGAAAAGCTGTTGACC 27

RESULT 14  
AP008212\_046/c

## WPCOMMENT

Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

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AP008212_003	300001	410000
AP008212_004	400001	510000
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AP008212_008	800001	910000
AP008212_009	900001	1010000
AP008212_010	1000001	1110000
AP008212_011	1100001	1210000
AP008212_012	1200001	1310000
AP008212_013	1300001	1410000
AP008212_014	1400001	1510000
AP008212_015	1500001	1610000
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Query Match 65.9%; Score 24.4; DB 4; Length 110000;  
Best Local Similarity 82.4%; Pred. No. 7;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
4 TGAATTCGGGCTGAAAAGCTTGTTCACC 37

DB 16436 TGAATCAGACCTTGAAGCTTGTTCACC 16403

RESULT 15  
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WPCOMMENT

Sequence split into 355 fragments LOCUS AP008210 Accession AP008210

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AP008210\_143 14300001 14410000  
AP008210\_144 14400001 14510000  
AP008210\_145 14500001 14610000  
AP008210\_146 14600001 14710000  
AP008210\_147 14700001 14810000  
AP008210\_148 14800001 14910000  
AP008210\_149 14900001 15010000  
AP008210\_150 15000001 15110000  
AP008210\_151 15100001 15210000  
AP008210\_152 15200001 15310000  
AP008210\_153 15300001 15410000  
AP008210\_154 15400001 15510000  
AP008210\_155 15500001 15610000  
AP008210\_156 15600001 15710000  
AP008210\_157 15700001 15810000  
AP008210\_158 15800001 15910000  
AP008210\_159 15900001 16010000  
AP008210\_160 16000001 16110000  
AP008210\_161 16100001 16210000  
AP008210\_162 16200001 16310000  
AP008210\_163 16300001 16410000  
AP008210\_164 16400001 16510000  
AP008210\_165 16500001 16610000  
AP008210\_166 16600001 16710000  
AP008210\_167 16700001 16810000  
AP008210\_168 16800001 16910000  
AP008210\_169 16900001 17010000  
AP008210\_170 17000001 17110000  
AP008210\_171 17100001 17210000  
AP008210\_172 17200001 17310000  
AP008210\_173 17300001 17410000  
AP008210\_174 17400001 17510000  
AP008210\_175 17500001 17610000  
AP008210\_176 17600001 17710000  
AP008210\_177 17700001 17810000  
AP008210\_178 17800001 17910000  
AP008210\_179 17900001 18010000  
AP008210\_180 18000001 18110000  
AP008210\_181 18100001 18210000  
AP008210\_182 18200001 18310000  
AP008210\_183 18300001 18410000  
AP008210\_184 18400001 18510000  
AP008210\_185 18500001 18610000  
AP008210\_186 18600001 18710000  
AP008210\_187 18700001 18810000  
AP008210\_188 18800001 18910000  
AP008210\_189 18900001 19010000  
AP008210\_190 19000001 19110000  
AP008210\_191 19100001 19210000  
AP008210\_192 19200001 19310000  
AP008210\_193 19300001 19410000  
AP008210\_194 19400001 19510000  
AP008210\_195 19500001 19610000  
AP008210\_196 19600001 19710000

Query Match 65.9%; Score 24.4; DB 4; Length 110000;  
Best Local Similarity 82.4%; Pred. No. 7;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 4 TCGAATTCGGCTGAAAAAGCGTTGACC 37  
Db 11954 TCGAATTCAGACTTGAAGAAAGCTTGTTGACC 11921

Search completed: May 19, 2006, 01:27:33  
Job time : 794.333 secs

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CC catalytic domain and a catalytic domain from an accessory enzyme that is  
 CC involved in formation of a nucleotide sugar which is a saccharide donor  
 CC for a glycosyltransferase reaction. The fusion protein is a saccharide donor  
 CC enzymatic synthesis of oligosaccharides. The fusion proteins are able to  
 CC catalyze more than one reaction involved in the enzymatic synthesis. This  
 CC is useful for the development of therapeutic agents that have specific  
 CC carbohydrate structures. Carbohydrates are involved in recognition  
 CC elements on the surface of cells. The fusion protein can be used for the  
 CC synthesis of both natural carbohydrates and synthetic derivatives with  
 CC novel properties. The fusion polypeptide allows two glycosyltransferase  
 CC reactions in a single vessel, provides improved yields of end products.  
 CC Additionally, cleanup and disposal of extra solvents and by-products is  
 CC reduced. The fusion protein can also use directly different donor  
 CC analogues and various acceptors with a terminal galactose residue

SQ Sequence 37 BP, 9 A, 6 C, 11 G, 11 T, 0 U, 0 Other;  
 Query Match 100.0%; Score 37; DB 2; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 2

AAA81515/c  
 ID AAA81515 standard; DNA; 16878 BP.

AC AAA81515;  
 DT 04-DEC-2000 (first entry)  
 DE N. meningitidis partial DNA sequence gum\_62 SEQ ID NO:62.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
 KM antigen; vaccine; diagnosis; infection; antibacterial; identification;  
 KW Meningococcus B; MenB; ds.

OS Neisseria meningitidis.

PN MO200022430-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99MO-US023573.

PR 09-OCT-1998; 98US-0103794P.

PR 30-APR-1999; 99US-0132068P.

PA (CHIR) CHIRON CORP.

PI Frazer CM, Hickey E, Peterson J, Tetzelin H, Venner JC,  
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scariselli M, Scarlato V;  
 PI Rapinoli R, Pizzo M;

DR WPI; 2000-318079/27.

PT Isolated nucleotide sequences of Neisseria meningitidis which can be used  
 PT in the diagnosis and treatment of N. meningitidis infection and other  
 PT Neisserial infections, for example, N. gonorrhoea.

PS Claim 7; Page 1385-1390, 1760pp; English.

CC The present invention describes methods of obtaining immunogenic proteins  
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent  
 CC specifically claimed Neisseria meningitidis genomic DNA sequences,  
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA  
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and  
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of  
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent  
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all

CC used in the exemplification of the present invention. The nucleic acid  
 CC sequences, protein sequences, and antibodies against them, can be used in  
 CC the manufacture of a composition. The composition can be used as a  
 CC medicament (or in the manufacture of a medicament) for treating,  
 CC preventing or diagnosing infection due to Neisserial bacteria. For  
 CC example, some of the identified proteins could be components of vaccines  
 CC against Meningococcus B, against all serotypes, and/or against all  
 CC pathogenic Neisseriae. Identification of sequences from the bacterium  
 CC will also facilitate production of biological probes, particularly  
 CC organism-specific probes. Attempts to make efficacious Meningococcus B  
 CC vaccines have failed mainly due to antigen tolerance. Multivalent  
 CC antigens have also been tried but none have successfully overcome  
 CC antigenic variability. The provision of further, complete sequences may  
 CC provide an opportunity to identify secreted or surface exposed proteins  
 CC that may be presumed targets for the immune system and which are not  
 CC antigenically variable or at least more conserved than other more  
 CC variable regions

SQ Sequence 16878 BP; 4598 A, 4598 C, 3853 G, 3827 T, 0 U, 2 Other;  
 Query Match 71.4%; Score 26.4; DB 3; Length 16878;  
 Best Local Similarity 96.4%; Pred. No. 1.3;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## RESULT 3

AAA81490\_09

Continuation (10 of 15) of AAA81490 from base 900001 (N. meningitidis B full length genom  
 WP Sequence split into 15 fragments LOCUS AAA81490 Accession AAA81490

WP	Fragment Name	Begin	End
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 71.4%; Score 26.4; DB 3; Length 110000;  
 Best Local Similarity 96.4%; Pred. No. 1.8;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 TCTGGGCTTGAAGGCTTGTGGAC 37  
 Db 34748 TATGGGCTTGAAGGCTTGTGGAC 34775

RESULT 4  
 ID AAF21609  
 AC AAF21609 standard; DNA; 349980 BP.

DT 13-MAR-2001 (first entry)

DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.

KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;  
 KM diagnosis; antigen; detection; infection; gene therapy; antibacterial;  
 ds.

```
OS Neisseria meningitidis.
XX
XX WO200066791-A1.
XX
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX 30-APR-1999; 99US-0132068P.
XX 08-OCT-1999; 99WO-US023573.
XX 28-FEB-2000; 2000GB-00004695.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tetelín H, Venter JC,
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarsella M, Scarlato V;
XX Rappoli R, Frazer CM, Grandi G;
XX
XX WPI; 2000-647603/62.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
XX frames are used to detect, treat and prevent Neisserial infections.
XX
XX Claim 7; Appendix A; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
XX meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
XX represent fragments of the NMB genomic sequence, as the sequence was too
XX long to go in a record on its own it was split into 8 sequences which
XX overlap each other at the beginning and end of each sequence by 49980 bp
XX (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
XX AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
XX AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
XX given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
XX primers which are used in the exemplification of the present invention.
XX The NMB genome and fragments from it have antibacterial activity, and can
XX be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
XX and/or antibodies which binds to the proteins can be used in compositions
XX for treating or preventing infection due to Neisserial bacteria or as a
XX diagnostic reagent for detecting the presence of Neisserial bacteria or
XX of antibodies raised to Neisserial bacteria. Computers, computer memory,
XX computer storage medium or computer databases can be used in a search to
XX identify open reading frames (ORFs) or coding sequences within the NMB
XX genome. The DNA sequences provide further opportunities to find antigenic
XX or immunogenic proteins which are more effective in vaccines than the
XX outer membrane proteins currently used
XX
XX Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 U; 0 Other;
SQ
Query Match 71.4%; Score 26.4; DB 3; Length 349980;
Best Local Similarity 96.4%; Pred. No. 2.3;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 10 TCTGGGCTTGAAGGCTTGTGACC 37
Db 34749 TATGGCTTGAAGGCTTGTGACC 34776
RESULT 5
AAFP21608
ID AAFP21608 standard; DNA; 349980 BP.
XX
XX AAFP21608;
XX
XX 13-MAR-2001 (first entry)
XX
XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX da.
XX
XX
```

```
OS Neisseria meningitidis.
XX
XX WO200066791-A1.
XX
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX 30-APR-1999; 99US-0132068P.
XX 08-OCT-1999; 99WO-US023573.
XX 28-FEB-2000; 2000GB-00004695.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tetelín H, Venter JC,
XX Masignani V, Galeotti C, Mora M, Ratti G, Scarsella M, Scarlato V;
XX Rappoli R, Frazer CM, Grandi G;
XX
XX WPI; 2000-647603/62.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
XX frames are used to detect, treat and prevent Neisserial infections.
XX
XX Claim 7; Appendix A; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
XX meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
XX represent fragments of the NMB genomic sequence, as the sequence was too
XX long to go in a record on its own it was split into 8 sequences which
XX overlap each other at the beginning and end of each sequence by 49980 bp
XX (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
XX AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
XX AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
XX given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
XX primers which are used in the exemplification of the present invention.
XX The NMB genome and fragments from it have antibacterial activity, and can
XX be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
XX and/or antibodies which binds to the proteins can be used in compositions
XX for treating or preventing infection due to Neisserial bacteria or as a
XX diagnostic reagent for detecting the presence of Neisserial bacteria or
XX of antibodies raised to Neisserial bacteria. Computers, computer memory,
XX computer storage medium or computer databases can be used in a search to
XX identify open reading frames (ORFs) or coding sequences within the NMB
XX genome. The DNA sequences provide further opportunities to find antigenic
XX or immunogenic proteins which are more effective in vaccines than the
XX outer membrane proteins currently used
XX
XX Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;
SQ
Query Match 71.4%; Score 26.4; DB 3; Length 349980;
Best Local Similarity 96.4%; Pred. No. 2.3;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 10 TCTGGGCTTGAAGGCTTGTGACC 37
Db 334749 TATGGCTTGAAGGCTTGTGACC 334776
RESULT 6
AAV04125
ID AAV04125 standard; DNA; 1116 BP.
XX
XX AAV04125;
XX
XX 17-JUN-1998 (first entry)
XX
XX N. meningitidis alpha-2,3-sialyltransferase DNA.
XX
XX Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid;
XX biologically active oligosaccharide; sialyl-modified protein; ss.
XX
XX Neisseria meningitidis.
XX
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XX Key Location/Qualifiers
FH CDS 1..116
FT /*tag= a
FT /product= "alpha-2,3-sialyl transferase"
PN MO9747749-A1.
XX
XX PD 18-DEC-1997.
XX PF 10-JUN-1997; 97WO-CA000390.
XX PR 10-JUN-1996; 96US-0019520P.
XX PR 07-JUN-1997; 97US-00872485.
XX PA (CANA ) NAT RES COUNCIL CANADA.
XX PI Gilbert M, Makarchuk WW, Young NM, Jennings MP,
XX DR WPI, 1998-05213/05.
XX DR P-PSDB; AAM41513.
XX
XX PT Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase -
XX PT useful to add sialic acid to acceptor with terminal galactose residue for
XX PT synthesis of biologically active oligosaccharide.
XX PS Claim 4; Page 37-38; 50pp; English.
XX
XX CC This sequence encodes an alpha-2,3-sialyltransferase which has been
XX CC isolated from Neisseria meningitidis. The protein can be used as a
XX CC reagent for adding a sialic acid residue to an acceptor having a terminal
XX CC galactose residue, e.g. in synthesis of biologically active
XX CC oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid
XX CC sequence can be used for the recombinant production of alpha-2,3-
XX CC sialyltransferase
XX
SQ Sequence 1116 BP; 306 A; 231 C; 292 G; 287 T; 0 U; 0 Other;
Query Match 70.3%; Score 26; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 12 TGGGCTTGAAAAAGGCTTGTGGACC 37
Db 2 TGGGCTTGAAAAAGGCTTGTGGACC 27

```

RESULT 7

AAH07120

ID AAH07120 standard; cDNA; 726 BP.

AC AAH07120;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA clone (5'-primer) SEQ ID NO:3955.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EPI074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

XX

PR 27-AUG-1999; 99JP-00300253.

XX

PR 11-JAN-2000; 2000JP-00118776.

XX

PR 02-MAY-2000; 2000JP-00183767.

XX

PR 09-JUN-2000; 2000JP-00241899.

XX

```

PA (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX PT length cDNAs defined in the specification, and for the detection and/or
XX PT diagnosis of the abnormality of the proteins encoded by the full-length
XX PT cDNAs.
XX
XX PS Claim 1; SEQ ID NO 3955; 2537p + Sequence listing; English.
XX
XX CC The present invention describes primer sets for synthesizing 5602 full-
XX CC length cDNAs defined in the specification, where a primer set comprises:
XX CC (a) an oligo-dT primer and an oligonucleotide complementary to the
XX CC complementary strand of a polynucleotide which comprises one of the 5602
XX CC oligonucleotide sequences defined in the specification, where the
XX CC or an oligonucleotide comprising a sequence complementary to the
XX CC complementary strand of a polynucleotide which comprises a 5'-end
XX CC sequence and an oligonucleotide comprising a sequence complementary to a
XX CC oligonucleotide which comprises a 3'-end sequence, where the
XX CC the 5'-end sequence/3'-end sequence is selected from those defined in the
XX CC specification. The primer sets can be used in antisense therapy and in
XX CC gene therapy. The primers are useful for synthesizing polynucleotides,
XX CC particularly full-length cDNAs. The primers are also useful for the
XX CC detection and/or diagnosis of the abnormality of the proteins encoded by
XX CC the full-length cDNAs. The primers allow obtaining of the full-length
XX CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
XX CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX CC present invention
XX
SQ Sequence 726 BP; 193 A; 171 C; 171 G; 188 T; 0 U; 3 Other;
Query Match 63.8%; Score 23.6; DB 4; Length 726;
Best Local Similarity 83.9%; Pred. No. 10;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 5 GGAATCTGGGCTTGAAAAAGGCTTGTGA 35
Db 633 GNACTTCGGGCTTAAAAAGACTTGCTGA 663

```

RESULT 8

ABL19064/C

ID ABL19064 standard; DNA; 2613 BP.

AC ABL19064;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8665.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US009231.

XX

PR 23-MAR-2000; 2000US-0191637P.

XX

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li FMD, Myers EM;  
XX WPI; 2001-656860/75.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell  
XX interactions.  
XX  
XX Claim 1; SEQ ID NO 8665; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signaling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
XX sequences (AB101840-AB116175) and the encoded proteins (AB57737-  
XX AB572072). The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_poc\_sequences  
XX  
XX Sequence 2613 BP; 796 A; 530 C; 543 G; 744 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 62.7%; Score 23.2; DB 4; Length 2613;  
XX Best Local Similarity 77.8%; Pred. No. 19;  
XX Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 GCATGGAATTCGGGCTTGAAAAAGCGTTGTTGAC 36  
Db 2436 GAATCGATTCTTAGGCTTTTCAAGGCTTGTTTAC 2401  
RESULT 9  
AB211361  
ID AB211361 standard; cDNA; 1734 BP.  
XX  
AC AB211361;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 243.  
XX  
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
XX cell-proliferative disorder; neurodegenerative disease; bacterial;  
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;  
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
XX arthritis; cytotoxic; immunomodulator; nootropic; neuroprotective;  
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
XX haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
XX antithratic; gene; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200270539-A2.  
XX PN  
XX 12-SEP-2002.  
XX PD  
XX 05-MAR-2002; 2002WO-US005095.  
XX PF  
XX 05-MAR-2001; 2001US-00799451.  
XX PR  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
XX PI Xue AY, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
XX PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
XX WPI; 2002-759812/82.  
XX DR P-PSDB; ABP69144.  
XX  
XX New polynucleotides comprising sequences assembled from expressed  
XX PT sequence tags (ESTs), useful for treating cell-proliferative,

PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
XX or coagulation disorders.  
XX  
XX Claim 1; SEQ ID NO 243; 1012pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising a  
XX nucleotide sequence selected from any of 948 sequences (AB21119-  
XX AB212066) or their mature protein coding portion, active domain coding  
XX protein or complementary sequences. The polynucleotides are useful for  
XX identifying expressed genes or for physical mapping of human genome. The  
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
XX markers, as a food supplement, for generating antibodies, in medical  
XX imaging, screening and diagnostic assays and for treating cell-  
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
XX arthritis, etc. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_poc\_sequences  
XX  
XX Sequence 1734 BP; 523 A; 385 C; 392 G; 434 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 62.2%; Score 23; DB 6; Length 1734;  
XX Best Local Similarity 83.9%; Pred. No. 22;  
XX Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 5 GGAATTCGGGCTTGAAAAAGCGTTGTTGA 35  
Db 589 GAATTCGGGCTTTAAAAAGACTTCTTCA 619  
RESULT 10  
ADM43879  
ID ADM43879 standard; cDNA; 1734 BP.  
XX  
AC ADM43879;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Novel human arginine-rich protein cDNA #243.  
XX  
XX ss; gene; human; arginine-rich protein; cancer; inflammation;  
XX genetic disorder.  
XX  
XX Homo sapiens.  
XX OS  
XX US2004053250-A1.  
XX PN  
XX 18-MAR-2004.  
XX PD  
XX 21-NOV-2002; 2002US-00302172.  
XX PF  
XX 05-MAR-2001; 2001US-00799451.  
XX PR 05-MAR-2002; 2002WO-US005095.  
XX PR 20-AUG-2002; 2002US-00225251.  
XX  
XX (TANG/) TANG Y T.  
XX PA (XUEA/) XUE A.  
XX PA (DRMA/) DRMANAC R T.  
XX  
XX Tang YT, Xue A, Drmanac RT;  
XX  
XX WPI; 2004-238579/22.  
XX DR  
XX New isolated arginine-rich protein-like polynucleotides and polypeptides,  
XX PT useful for diagnosing and/or treating conditions associated with aberrant  
XX PT activity of the arginine-rich polypeptides, such as cancer and  
XX PT inflammation.  
XX  
XX Disclosure; SEQ ID NO 243; 51pp; English.  
XX PS

CC The invention relates to an isolated polynucleotide. The methods and  
 CC compositions of the present invention are useful for the diagnosis and/or  
 CC treatment of diseases or conditions associated with aberrant expression  
 CC or activity of the arginine-rich protein-like polypeptides, such as  
 CC cancer and inflammation. They can also be used in forensics, gene  
 CC mapping, identification of mutations responsible for genetic disorders,  
 CC and in assessing biodiversity. The present sequence represents a novel  
 CC human arginine-rich protein cDNA.

SO Sequence 1734 BP; 523 A; 385 C; 392 G; 434 T; 0 U; 0 Other;

Query Match 62.2%; Score 23; DB 12; Length 1734;  
 Best Local Similarity 83.9%; Pred. No. 22;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGA 35  
 Db 569 GAACCTTCGGGCTTGAAGAGCTTGTGA 619

RESULT 11

AAH16361  
 ID AAH16361 standard; cDNA; 2228 BP.

AC AAH16361;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:15295.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

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CC Gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893  
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent  
 CC oligonucleotides, all of which are used in the exemplification of the  
 CC present invention

SO Sequence 2228 BP; 662 A; 462 C; 474 G; 630 T; 0 U; 0 Other;

Query Match 62.2%; Score 23; DB 4; Length 2228;  
 Best Local Similarity 83.9%; Pred. No. 23;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGA 35  
 Db 633 GAACCTTCGGGCTTGAAGAGCTTGTGA 663

RESULT 12

AD084099  
 ID AD084099 standard; cDNA; 2228 BP.

AC AD084099;

DT 07-OCT-2004 (first entry)

DE Human tumour-associated antigenic target (TAT) cDNA sequence #913.

human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;

XX cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-041988P.

XX (GETH ) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

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The present invention describes an isolated tumour-associated antigenic

target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of

(a); (c) the complement of (a) or (b); (d) a sequence that has 80%

sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -

(c). Also described: (1) an expression vector comprising the above

nucleic acid; (2) a host cell comprising the above expression vector; (3)

a process for producing a polypeptide; (4) an isolated polypeptide

comprising: (a) an amino acid sequence encoded by any of the above

nucleotide sequences; (b) an amino acid sequence encoded by the full-

length coding region of the above nucleotide sequences; or (c) a sequence

comprising the above polypeptide fused to a heterologous polypeptide; (6)

an isolated antibody that binds to the above polypeptide; (7) a process

for producing the antibody; (8) an isolated oligopeptide that binds to

the above polypeptide; (9) a tumour-associated antigenic target (TAT)

CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide;  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.

XX  
 SQ Sequence 2228 BP; 663 A; 460 C; 475 G; 630 T; 0 U; 0 Other;  
 Query Match 62.2%; Score 23; DB 12; Length 2228;  
 Best Local Similarity 83.9%; Pred. No. 23;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAATCTGGGCTGAAAAGGCTTGTGA 35  
 |||||  
 Db 633 GAACTTCTGGGCTTTAAAAGACTTGTGA 663

RESULT 13  
 AAL61230  
 ID AAL61230 standard; CDNA; 2942 BP.  
 AC AAL61230;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE Human secreted protein (SECP)-1 cDNA.  
 XX  
 KM Human; secreted protein; SECP; neurodegenerative disorder; scleroderma;  
 KM Parkinson's disease; Alzheimer's disease; myotonic dystrophy; leukaemia;  
 KM muscular disorder; systemic lupus erythematosus; renal disorder; cancer;  
 KM immunological disorder; gastrointestinal disorder; catatonias; infection;  
 KM diabetes; Goodpasture's syndrome; cardiovascular disorder; gene therapy;  
 KM endocrine disorder; atherosclerosis; transgenic animal; Grave's disease;  
 KM allergy; Crohn's disease; hepatic disease; cirrhosis; transgenic; gene;  
 ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 232..2133  
 FT /tag= a  
 FT /product= "Human SECP protein"  
 XX  
 PN WO2003046196-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 21-NOV-2002; 2002WO-US037803.  
 XX  
 PR 28-NOV-2001; 2001US-0334229P.  
 PR 07-DEC-2001; 2001US-0339236P.  
 PR 21-DEC-2001; 2001US-0343555P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Baughn MR, Becha SD, Chawla NK, Emerling BM, Fu G, Ison CH;

PI Jin P, Kabie AE, Lal PG, Lee S, Marguis JP, Lehr-Mason PM;  
 PI Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Wang JT, Warren BA;  
 PI Yue H, Zebbarjadian Y, Das D;  
 XX  
 DR WPI; 2003-505207/47.  
 DR P-PSDB; AAO30398.  
 XX  
 PT New SECP polypeptides, useful for diagnosing, preventing, and treating  
 PT disorders associated with an abnormal expression or activity of SECP,  
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer  
 PT and/or infections.  
 XX  
 PS Claim 5; Page 170-171; 194pp; English.

XX  
 CC The invention relates to human secreted proteins (SECP) and nucleic acid  
 CC molecules encoding such proteins. SECP sequences are useful in  
 CC diagnosing, preventing and treating disorders associated with an abnormal  
 CC expression or activity of SECP such as neurodegenerative disorders (e.g.  
 CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.  
 CC myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes,  
 CC Grave's disease), cancers (e.g. leukaemia, cervical or breast cancer),  
 CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,  
 CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal  
 CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, fungal,  
 CC bacterial, parasitic, protozoal, helminthic), cardiovascular disorders  
 CC (e.g. atherosclerosis) or hepatic diseases (e.g. cirrhosis). SECP  
 CC polynucleotides can be used to create humanised animals or transgenic  
 CC animals to model human disease. The invention is useful in gene therapy.  
 CC The present sequence is human SECP protein encoding cDNA

XX  
 SQ Sequence 2942 BP; 883 A; 624 C; 656 G; 779 T; 0 U; 0 Other;  
 Query Match 62.2%; Score 23; DB 9; Length 2942;  
 Best Local Similarity 83.9%; Pred. No. 24;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAATCTGGGCTGAAAAGGCTTGTGA 35  
 |||||  
 Db 613 GAACTTCTGGGCTTTAAAAGACTTGTGA 643

RESULT 14  
 AAX10673/c  
 ID AAX10673 standard; DNA; 225 BP.  
 XX  
 AC AAX10673;  
 XX  
 DT 30-MAR-1999 (first entry)  
 XX  
 DE Human biallelic polymorphic DNA fragment WI-6315.  
 XX  
 KM Polymorphism; biallelic; human; forensic; paternity testing; disease;  
 KM detection; phenotypic typing; characteristic; infection; hereditary;  
 KM autoimmune disease; cancer; inflammation; drug; therapy; medicament;  
 KM treatment; marker; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 232..2133  
 FT /tag= a  
 FT /product= "Human SECP protein"  
 XX  
 PN WO9820165-A2.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 05-NOV-1997; 97WO-US020313.  
 XX  
 PR 06-NOV-1996; 96US-0030455P.  
 XX  
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Lander ES, Wang D, Hudson T;  
 XX  
 DR WPI; 1998-286974/25.  
 XX  
 PT New isolated nucleic acid segments from the human genome - used for

PT determining polymorphic forms for use in e.g. forensics, paternity  
 testing or phenotypic typing for disease.

Claim 1, Page 70, 310pp, English.

AA10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases

SQ Sequence 225 BP; 55 A; 51 C; 46 G; 72 T; 0 U; 1 Other;

Query Match 61.6%; Score 22.8; DB 2; Length 225;  
 Best Local Similarity 79.4%; Pred. No. 18;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 GCATGGAATTCGTGGCTTGAAGGCTGTTG 34  
 DB 100 GCATGACACGCTGGCTTGAAGGACCTGTTG 67

RESULT 15

AA10672/c  
 ID AAX10672 standard; DNA; 225 BP.

AC AAX10672;

DT 30-MAR-1999 (first entry)

DE Human biallelic polymorphic DNA fragment WI-6315b.

KW Polymorphism; biallelic; human; forensic; paternity testing; disease;  
 detection; phenotypic typing; characteristic; infection; hereditary;  
 autoimmune disease; cancer; inflammation; drug; therapy; medication;  
 treatment; marker; ss.

OS Homo sapiens.

PN MO9820165-A2.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US020313.

PR 06-NOV-1996; 96US-0030455P.

PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

PI Lander ES, Wang D, Hudson T;

DR WPI; 1998-286974/25.

PT New isolated nucleic acid segments from the human genome - used for  
 determining polymorphic forms for use in e.g. forensics, paternity  
 testing or phenotypic typing for disease.

PS Claim 1, Page 70, 310pp, English.

CC AAX10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases

SQ Sequence 225 BP; 55 A; 50 C; 46 G; 73 T; 0 U; 1 Other;

Query Match 61.6%; Score 22.8; DB 2; Length 225;  
 Best Local Similarity 79.4%; Pred. No. 18;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 GCATGGAATTCGTGGCTTGAAGGCTGTTG 34  
 DB 100 GCATGACACGCTGGCTTGAAGGACCTGTTG 67

Search completed: May 19, 2006, 00:53:17  
 Job time : 180.906 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 00:53:30 ; Search time 1485.78 Seconds

(without alignments)  
1392.544 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37  
Sequence: 1 gcatggaattctgggcttgaagaaagctgttacc 37

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gsa1:\*  
12: gb\_gsa2:\*  
13: gb\_gsa3:\*  
14: gb\_gsa4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25.8	69.7	901	4 A1325176	A1325176 ms01h12.x
2	25.4	68.6	618	4 C80292	C80292 C80292 Mous
3	24.4	65.9	1443	13 CL969122	CL969122 OsIFCC017
4	24.4	65.9	1446	13 CL970741	CL970741 OsIFCC020
5	24	64.9	663	7 BB642392	BB642392 BB642392
C 6	23.8	64.3	635	5 CF295692	CF295692 300GS--05
7	23.8	64.3	828	5 CR109858	CR109858 Forward s
8	23.8	64.3	843	14 CR207976	CR207976 Forward s
9	23.8	64.3	884	14 CR226869	CR226869 Forward s
10	23.8	64.3	912	14 CR050996	CR050996 Forward s
11	23.6	63.8	726	1 AUI33964	AUI33964 Forward s
12	23.4	63.2	725	11 A2192473	A2192473 SP 1021 B
13	23.2	62.7	663	2 B1096984	B1096984 SCUM32-DS
14	23	62.2	453	2 BF744479	BF744479 OV2-BT063
15	23	62.2	498	12 CG614466	CG614466 OST302754
16	23	62.2	507	9 DB047668	DB047668 DB047668
17	23	62.2	518	9 DB021107	DB021107 DB021107
18	23	62.2	527	12 CG596353	CG596353 OST258118
19	23	62.2	530	9 DB056413	DB056413 DB056413

20	23	62.2	563	9 DB049403	DB049403
21	23	62.2	565	9 DB051314	DB051314
22	23	62.2	566	9 DB031260	DB031260
23	23	62.2	567	7 AW962292	AW962292 EST374365
24	23	62.2	574	9 DB039479	DB039479
25	23	62.2	578	9 DB031132	DB031132 DB031132
26	23	62.2	600	8 CV024531	CV024531 1931 Full1
27	23	62.2	674	7 BB617250	BB617250 BB617250
28	23	62.2	685	2 BG773112	BG773112 602722833
29	23	62.2	698	4 BY171855	BY171855 BY171855
30	23	62.2	709	7 BB615455	BB615455 BB615455
31	23	62.2	815	5 C1488602	C1488602 C1488602
32	23	62.2	818	2 BG771738	BG771738 602720406
C 33	23	62.2	822	14 CR040392	CR040392 Forward s
C 34	23	62.2	832	5 CD632278	CD632278 56049046H
35	23	62.2	1891	14 AY404519	AY404519 Mus muscu
36	23	62.2	1911	14 AY404517	AY404517 Homo sap1
37	23	62.2	1911	14 AY404518	AY404518 Pan trogl
38	23	62.2	1928	6 AK037169	AK037169 Mus muscu
39	23	62.2	1976	6 AK044441	AK044441 Mus muscu
40	23	62.2	2224	6 AK020021	AK020021 Mus muscu
41	23	62.2	2393	6 AK029724	AK029724 Mus muscu
42	23	62.2	3455	6 AK033409	AK033409 Mus muscu
C 43	22.8	61.6	226	10 Z38338	Z38338 HSC078032 n
C 44	22.8	61.6	366	10 T15936	T15936 IB2156 Intfa
C 45	22.8	61.6	464	4 BX103153	BX103153 BX103153

#### ALIGNMENTS

RESULT 1  
A1325176/c 901 bp mRNA linear EST 23-DEC-1998  
LOCUS  
DEFINITION  
ms01h12.x1 Stratagene mouse embryonic carcinoma (#937317) Mus  
muscle cDNA clone IMAGE:605735 3' similar to gb:D16141 Mouse  
mgl-1 mRNA for ORF, complete cds (MOUSE), mRNA sequence.

ACCESSION  
A1325176  
VERSION  
A1325176.1 GI:4059605  
KEYWORDS  
EST.  
SOURCE  
Mus musculus  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE  
JOURNAL  
COMMENT  
The WashU-HMNI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HMNI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.wustl.edu  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1371167  
This clone was previously sequenced on the 5' end only, this new  
data is from the 3' end  
High quality sequence stop: 432.  
Location/Qualifiers  
1..901  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:605735"  
/issue\_type="carcinoma"

FEATURES  
source

/dev stage="embryonic"  
/lab host="SOLR (kanamycin resistant)"  
/clone\_lib="Stratagene mouse embryonic carcinoma  
(#937317)"  
/note="vector: plusescript SK-; Site 1: EcoRI, site 2:  
XhoI; Cloned unidirectionally. Primer: Oligo dT. p19 cell  
line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'  
adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor  
sequence: 5' CTCGAGTTT TTTT TTTT TTTT 3'."

## ORIGIN

Query Match 69.7%; Score 25.8; DB 1; Length 901;  
Best Local Similarity 81.1%; Pred. No. 17;  
Matches 30; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCATGAATTCCTGGCTTGAAGGCTTGTGACC 37  
Db 823 GCATGAATTCCTGGCTTGAAGGCTTGTGACC 787

## RESULT 2

## LOCUS

CG0292 618 bp mRNA linear EST 26-JUN-1998  
DEFINITION C80292 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone

VERSION J0079C07 3' similar to Human mRNA for KIAA0312 gene, mRNA sequence.  
C80292  
C80292.1 GI:2520622

EST.  
Mus musculus (house mouse)

Mus musculus  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 618)  
Ko, M.S.H., Kitchen, J.R., Wang, X., Wang, X., Threat, T.A., Sun, T.,  
Grabovac, M.J., Mason, S., Lim, M.K., Paonessa, P.D., Sauls, A.D. and  
Doi, H.

## REFERENCE

## AUTHORS

## TITLE

Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst  
(The ERATO/Doi Project at Wayne State University)

## JOURNAL

Unpublished (1997)  
Contact: Hirofumi Doi

Doi Biosymmetry Project, ERATO  
Japan Science and Technology Corporation (JST)  
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan  
Email: hdo@doi.jst.go.jp.

Location/Qualifiers  
1. 618

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="J0079C07"  
/tissue\_type="Blastocyst"  
/dev\_stage="3.5-dpc"  
/clone\_lib="Mouse 3.5-dpc blastocyst cDNA"

## FEATURES

## source

ORIGIN  
Query Match 69.7%; Score 25.4; DB 4; Length 618;  
Best Local Similarity 82.9%; Pred. No. 22;  
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ATGAATTCCTGGCTTGAAGGCTTGTGACC 37  
Db 576 ATGAATTCCTGGCTTGAAGGCTTGTGACC 610

RESULT 3  
LOCUS CL969122 1443 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC017869 Oryza sativa Expressed Library Oryza sativa (indica  
cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL969122  
VERSION CL969122.1 GI:52392873

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

GSS.  
Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP  
1 (bases 1 to 1443)  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
Wong, G.K.S., Deng, X.W. and Wang, J.  
An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis  
Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80486676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.

## FEATURES

## source

/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Expressed Library"  
/note="Oryza sativa exon trapped genomic sequences"

## ORIGIN

Query Match 65.9%; Score 24.4; DB 13; Length 1443;  
Best Local Similarity 82.4%; Pred. No. 70;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 TGAATTCCTGGCTTGAAGGCTTGTGACC 37  
Db 532 TGAATTCCTGGCTTGAAGGCTTGTGACC 565

## RESULT 4

## LOCUS

CL970741 1446 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC020412 Oryza sativa Expressed Library Oryza sativa (indica  
cultivar-group) genomic, genomic survey sequence.  
CL970741  
CL970741.1 GI:52396091

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP  
1 (bases 1 to 1446)  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
Wong, G.K.S., Deng, X.W. and Wang, J.  
An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis  
Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomic  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80486676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers  
1. 1446  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"

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/db_xref="taxon:39946"
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Best Local Similarity 82.4%; Pred. No. 70;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy      4 TGAATTCTGGGCTTGAAGGCTTTGACC 37
         ||||| ||||| ||||| ||||| |||||
Db      532 TGAATGACGAGCTTGAAGGCTTTGTTGACC 565

RESULT 5
BB642392
LOCUS
DEFINITION
BB642392 RIKEN full-length enriched, adult retina Mus musculus cDNA
clone A930013F09 5', mRNA sequence.
BB642392
VERSION
BB642392.1 GI:16477311
SOURCE
Mus musculus (house mouse)
KEYWORDS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 663)
REFERENCE
AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Kono,H., Konda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Haysishizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
TITLE
Contact: Yoshinide Haysishizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/
COMMENT
Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Haysishizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Oawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Haysishizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Haysishizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Haysishizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
source
1. .663
Location/Qualifiers
/organism="Mus musculus"

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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A930013F09"
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/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult retina"
/note="Site 1: Salt; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTTTTATTTTATTTTATTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5'GAGAGAGATTCGATTCGATTATTAATTATTCCTCCCTCCCTCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. -Retina RNA was provided by Stefano Guerinich,
Department of Neurobiology, Harvard Medical School, 220
Longwood Ave., Boston, MA02115, USA, whose assistance we
gratefully acknowledge."
ORIGIN
Query Match      64.9%; Score 24; DB 7; Length 663;
Best Local Similarity 84.4%; Pred. No. 86;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy      4 TGAATTCTGGGCTTGAAGGCTTTGTTGA 35
         ||||| ||||| ||||| ||||| |||||
Db      567 TGAATCTGCGGTTAAAGAGCTTTGGA 598

RESULT 6
CF295692/c
LOCUS
DEFINITION
CF295692 635 bp mRNA linear EST 14-AUG-2003
30DGS-05-L22.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS-05-L22, mRNA
sequence.
CF295692
VERSION
CF295692.1 GI:33664725
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 635)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .635
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="30 days after germination"

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/lab host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
 /note=Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

## ORIGIN

Query Match 64.3%; Score 23.8; DB 5; Length 635;  
 Best Local Similarity 80.0%; Pred. No. 1e+02;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 ATGGAATTCGGGCTTGAAGGCTTGTGGAC 37  
 Db 211 ATGGAATTCGGCTGGAAGGCTTGTGGCC 177

RESULT 7 CR109858 828 bp DNA linear GSS 05-JUL-2004  
 LOCUS Forward strand read from insert in 5'HPRT insertion targeting and  
 CR109858 chromosome engineering clone MHPN180g24, genomic survey sequence.

ACCESSION CR109858.1 GI:49857273  
 VERSION GSS; genome survey sequence; MICER.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 828)  
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.  
 AUTHORS

TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
 FEATURES Location/Qualifiers

source  
 1..828  
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## ORIGIN

Query Match 64.3%; Score 23.8; DB 14; Length 828;  
 Best Local Similarity 80.0%; Pred. No. 1e+02;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGGCTTGAAGGCTTGTGGA 35  
 Db 656 GCATGAATTCGTGTTGAATATATCGTTGA 690

RESULT 8 CR207976 843 bp DNA linear GSS 06-JUL-2004  
 LOCUS Forward strand read from insert in 5'HPRT insertion targeting and  
 CR207976 chromosome engineering clone MHPN184k16, genomic survey sequence.

ACCESSION CR207976.1 GI:4986825  
 VERSION GSS; genome survey sequence; MICER.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 843)  
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.  
 AUTHORS

TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
 Location/Qualifiers

## FEATURES

source  
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Query Match 64.3%; Score 23.8; DB 14; Length 843;  
 Best Local Similarity 80.0%; Pred. No. 1e+02;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGGCTTGAAGGCTTGTGGA 35  
 Db 648 GCATGAATTCGTGTTGAATATATCGTTGA 682

RESULT 9 CR126869 884 bp DNA linear GSS 06-JUL-2004  
 LOCUS Forward strand read from insert in 5'HPRT insertion targeting and  
 CR126869 chromosome engineering clone MHPN78a07, genomic survey sequence.

ACCESSION CR126869.1 GI:49874321  
 VERSION GSS; genome survey sequence; MICER.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 884)  
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.  
 AUTHORS

TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
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 Best Local Similarity 80.0%; Pred. No. 1e+02;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGGCTTGAAGGCTTGTGGA 35  
 Db 656 GCATGAATTCGTGTTGAATATATCGTTGA 690

RESULT 10 CR050996 912 bp DNA linear GSS 05-JUL-2004  
 LOCUS Forward strand read from insert in 5'HPRT insertion targeting and  
 CR050996 chromosome engineering clone MHPN71g17, genomic survey sequence.

ACCESSION CR050996.1 GI:49784135  
 VERSION GSS; genome survey sequence; MICER.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 912)  
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.  
 AUTHORS

TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

TITLE Rogers, J. and Bradley, A.  
JOURNAL Direct Submission (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>  
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Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGGAATTCCTGGCTGAAAAGGCTTGTGA 35  
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661 GCATGGAATTCCTGGCTTGAATATATCTTTGA 695  
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RESULT 11  
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LOCUS AUI33964 OVARC1 Homo sapiens cDNA clone OVARC1001010 5', mRNA  
DEFINITION  
sequence.  
ACCESSION AUI33964  
VERSION AUI33964.1 GI:10994503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 726)  
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,  
Yamashita, R., Yamamoto, J., Sekine, M., Isuritani, K., Wakaguri, H.,  
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,  
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuna, M.,  
Murakawa, K., Ishida, S., Iehibashi, T., Takahashi-Fujii, A.,  
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
JOURNAL Contact: Takao Isogai  
PUBMED FRI Project (HRI Team)  
COMMENT Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: fli-cdn@hri.com  
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.  
FEATURES  
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1..726  
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/clone="OVARC1001010"  
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QY 5 GAATTCGGGCTTGAAAAGGCTTGTGA 35  
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Db 633 GNACTTCGGGCTTTAAAGAACTTGTCTGA 663  
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RESULT 12  
A2192473 725 bp DNA linear GSS 30-AUG-2000  
LOCUS A2192473  
DEFINITION SP-1021.B1.E08.SP6E Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
genomic clone Plate=1021 Col=15 Row=J, genomic survey sequence.  
A2192473  
ACCESSION A2192473 GI:8375752  
VERSION A2192473  
KEYWORDS GSS.  
SOURCE Strongylocentrotus purpuratus  
ORGANISM Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Echinoidea; Echinacea; Echinoidea;  
Strongylocentrotidae; Strongylocentrotus.  
1 (bases 1 to 725)  
Cameron, R.A., Mahatras, G., Rast, J.P., Martinez, P., Biondi, T.R.,  
Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T.,  
Wray, G.A., Eitensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H.  
and Hood, L.  
A sea urchin genome project: Sequence scan, virtual map, and  
additional resources  
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
10920195  
Contact: Cameron, RA, Davidson, EH, Hood, L  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu  
Plate: 1021 row: J column: 15  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 725.  
FEATURES  
source  
1..725  
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/db\_xref="taxon:7668"  
/clone="Plate=1021 Col=15 Row=J"  
/clone\_1db="Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library"  
/note="Organ: sperm; Vector: BACs; BAC Clones in E-Coli  
DH10B"

ORIGIN  
Query Match 63.2%; Score 23.4; DB 11; Length 725;  
Best Local Similarity 81.8%; Pred. No. 1.6e+02;  
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCATGGAATTCCTGGCTGAAAAGGCTTGT 33  
|||||  
Db 360 GCATGCCATTCCTGGCCAGAAAAGGCTGTAT 392  
|||||

RESULT 13  
B1096984 663 bp mRNA linear EST 25-JUN-2001  
LOCUS B1096984  
DEFINITION SCUM32-DB1-1 Melaleuca alternifolia (Cheel) mRNA Melaleuca  
alternifolia cDNA, mRNA sequence.  
B1096984  
ACCESSION B1096984 GI:14548641  
VERSION B1096984.1  
KEYWORDS EST.  
SOURCE Melaleuca alternifolia (tea tree)  
ORGANISM Melaleuca alternifolia  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Myrtales; Myrtaceae; Melaleuca.

REFERENCE 1 (bases 1 to 663)  
 AUTHORS Shelton,D., Leach,D., Beverstock,P and Henry,R.  
 TITLE Isolation of genes involved in secondary metabolism from *Melaleuca alternifolia* (Cheel) using expressed sequence tags (ESTs)  
 JOURNAL Plant Sci. 162 (1), 9-15 (2002)  
 COMMENT Contact: Shelton D  
 Centre for Plant Conservation Genetics  
 Southern Cross University  
 P.O. Box 157, Lismore, NSW 2480, Australia  
 Tel: 61 2 6620 3173  
 Fax: 61 2 6622 2080  
 Email: dshelton@scu.edu.au.

FEATURES  
 source Location/Qualifiers  
 1..663  
 /organism="Melaleuca alternifolia"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:164405"  
 /clone\_lib="Melaleuca alternifolia (Cheel) mRNA"

ORIGIN  
 Query Match 62.7%; Score 23.2; DB 2; Length 663;  
 Best Local Similarity 75.7%; Pred. No. 1.9e+02;  
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCATGAATTCCTGGCGCTTGAAGAGCTGTGTTGACC 37  
 345 GCTTGAATTCGAGACTTGAGAGCGCTTGTGTTTACC 381

Db

RESULT 14  
 Bf744479 453 bp mRNA linear EST 10-JAN-2001  
 LOCUS QV2-BT0636-291000-443-a01 BT0636 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION Bf744479  
 VERSION Bf744479.1 GI:12071155  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 453)  
 Dias Neco,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
 JOURNAL  
 PUBMED  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&ct=QV2-BT0636-291000-443-a01&ct3=2000-10-29&ct4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 453.

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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="BT0636"

/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN  
 Query Match 62.2%; Score 23; DB 2; Length 453;  
 Best Local Similarity 83.9%; Pred. No. 2.1e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTGTGTTGA 35  
 378 GAACCTTCGGGCTTTAAAAAGACTTGCTTGA 408

Db

RESULT 15  
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 LOCUS OSTR302754 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR302754,  
 DEFINITION mRNA sequence.  
 ACCESSION CG614466  
 VERSION CG614466.1 GI:37438315  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 498)  
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richer,L.J., Piggott,J., Beltrande-Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhautf,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,W.J., Van Slijtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Pearson,C. and Sands,A.T.  
 Mx1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 14610273  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap

## JOURNAL

## PUBMED

## COMMENT

## FEATURES

## source

Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OSTR302754"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

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 Best Local Similarity 83.9%; Pred. No. 2.1e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTGTGTTGA 35  
 Db 408 GAACCTTCGGGCTTTAAAAAGACTTGCTTGA 438

Search completed: May 19, 2006, 02:31:54  
 Job time : 1489.78 secs

Fri May 19 11:37:23 2006

us-09-211-691-5.rst

Page 7

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 01:27:44 ; Search time 59.3542 Seconds  
(without alignments)  
1166.405 Million cell updates/sec

Title: US-09-211-691-5

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Sequence: 1 gcacggacatctggcgctgaaagcgtcttgcacc 37

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	70.3	1116	US-08-872-485-1	Sequence 1, Appl1
2	26	70.3	1116	US-09-387-942-1	Sequence 1, Appl1
3	23	62.2	1734	US-09-799-451-243	Sequence 243, App
4	21	56.8	62873	US-09-949-016-15676	Sequence 15676, A
5	21	56.8	222452	US-09-949-016-12968	Sequence 12968, A
6	20.8	56.2	1022	US-09-257-584-5	Sequence 5, Appl1
7	20.8	56.2	1023	US-09-257-584-4	Sequence 4, Appl1
8	20.8	56.2	2546	US-09-598-401C-95	Sequence 95, Appl1
9	20.2	54.6	601	US-09-949-016-35388	Sequence 35388, A
10	20.2	54.6	601	US-09-949-016-35389	Sequence 35389, A
11	20.2	54.6	601	US-09-949-016-44447	Sequence 44447, A
12	20.2	54.6	601	US-09-949-016-44448	Sequence 44448, A
13	20.2	54.6	679	US-09-533-559-5172	Sequence 5172, App
14	20.2	54.6	50810	US-09-949-016-16039	Sequence 16039, A
15	20.2	54.6	54452	US-09-949-016-12642	Sequence 12642, A
16	20.2	54.6	54452	US-09-949-016-13003	Sequence 13003, A
17	20.2	54.6	60465	US-09-949-016-15995	Sequence 15995, A
18	20	54.1	590	US-09-533-559-2554	Sequence 2554, App
19	20	54.1	601	US-09-949-016-84389	Sequence 84389, A
20	20	54.1	601	US-09-949-016-84390	Sequence 84390, A
21	20	54.1	18798	US-09-949-016-17531	Sequence 17531, A
22	20	54.1	59158	US-09-949-002-728	Sequence 728, App
23	20	54.1	64994	US-09-949-002-688	Sequence 688, App

C	24	20	54.1	94618	4	US-09-531-120-191	Sequence 191, App
C	25	20	54.1	94987	3	US-09-949-016-12510	Sequence 12510, A
C	26	20	54.1	105210	3	US-09-949-016-14158	Sequence 14158, A
C	27	20	54.1	786431	3	US-09-751-389-3	Sequence 3, Appl1
C	28	19.8	53.5	507	3	US-09-621-976-18901	Sequence 18901, A
C	29	19.6	53.0	252	3	US-09-513-999C-28576	Sequence 28576, A
C	30	19.6	53.0	1116	3	US-08-872-485-3	Sequence 3, Appl1
C	31	19.6	53.0	1116	3	US-09-387-942-1	Sequence 3, Appl1
C	32	19.6	53.0	19446	3	US-08-961-527-51	Sequence 51, Appl1
C	33	19.6	53.0	68444	3	US-09-949-016-13968	Sequence 13968, A
C	34	19.6	53.0	107827	3	US-09-949-016-15790	Sequence 15790, A
C	35	19.6	53.0	265038	3	US-09-949-016-15779	Sequence 15779, A
C	36	19.4	52.4	601	3	US-09-949-016-34056	Sequence 34056, A
C	37	19.4	52.4	601	3	US-09-949-016-34057	Sequence 34057, A
C	38	19.4	52.4	601	3	US-09-949-016-140221	Sequence 140221, A
C	39	19.4	52.4	601	3	US-09-949-016-140222	Sequence 140222, A
C	40	19.4	52.4	1389	2	US-08-426-428-1	Sequence 1, Appl1
C	41	19.4	52.4	1389	2	US-08-871-314-1	Sequence 1, Appl1
C	42	19.4	52.4	1838	3	US-09-949-016-261	Sequence 261, App
C	43	19.4	52.4	1838	3	US-09-949-016-1435	Sequence 1435, App
C	44	19.4	52.4	1838	4	US-09-880-107-3813	Sequence 3813, App
C	45	19.4	52.4	1899	3	US-09-919-039-153	Sequence 153, App

#### ALIGNMENTS

RESULT 1  
US-08-872-485-1  
Sequence 1, Application US/08872485  
Patent No. 6096529  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Wakarchuk, Warren W.  
APPLICANT: Young, N. Martin  
APPLICANT: Jennings, Michael P.  
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases  
TITLE OF INVENTION: and Their Uses  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/872,485  
FILING DATE: 07-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,520  
FILING DATE: 10-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 014137-012000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1116 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:

ORGANISM: Neisseria meningitidis  
STRAIN: 406Y, NRCC 4030  
INDIVIDUAL ISOLATE: Capsule type: Y; lipooligosaccharide  
INDIVIDUAL ISOLATE: type: L3  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1116  
OTHER INFORMATION: /product= "alpha-2,3-sialyltransferase"  
US-08-872-485-1

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Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCTTTGACC 37  
DB 2 TGGGCTTGAAAAAGCTTTGACC 27

RESULT 2  
US-09-387-942-1  
Sequence 1, Application US/09387942  
Patent No. 6210933

GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Wakarchuk, Warren W.  
APPLICANT: Young, N. Martin  
TITLE OF INVENTION: Jemmings, Michael P.  
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,942  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/872,485  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 014137-012000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1116 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Neisseria meningitidis  
STRAIN: 406Y, NRCC 4030  
INDIVIDUAL ISOLATE: Capsule type: Y; lipooligosaccharide  
INDIVIDUAL ISOLATE: type: L3  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1116  
OTHER INFORMATION: /product= "alpha-2,3-sialyltransferase"

US-09-387-942-1

Query Match 70.3%; Score 26; DB 3; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCTTTGACC 37  
DB 2 TGGGCTTGAAAAAGCTTTGACC 27

RESULT 3  
US-09-799-451-243  
Sequence 243, Application US/09799451  
Patent No. 6783969

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie  
APPLICANT: Xue, Aidong J.  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Ma, Yungang  
APPLICANT: Yamazaki, Victoria  
APPLICANT: Chen, Rui-hong  
APPLICANT: Wang, Zhiwei  
APPLICANT: Yang, Yonghong  
APPLICANT: Wehrman, Tom  
APPLICANT: Ghosh, Reena  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 803  
CURRENT APPLICATION NUMBER: US/09/799,451  
CURRENT FILING DATE: 2001-03-05  
NUMBER OF SEQ ID NOS: 948  
SOFTWARE: pc\_FL\_genes Version 2.0  
SEQ ID NO 243  
LENGTH: 1734  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (208) ..(1695)  
US-09-799-451-243

Query Match 62.2%; Score 23; DB 3; Length 1734;  
Best Local Similarity 83.9%; Pred. No. 7.4;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAATTCGGGCTTGAAAAAGCTTTGA 35  
DB 589 GAACTTCGGGCTTTAAAAAGACTTGCTGA 619

RESULT 4  
US-09-949-016-15676/C  
Sequence 15676, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C0001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15676  
LENGTH: 62873  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1) .. (62873)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15676

Query Match 56.8%; Score 21; DB 3; Length 62873;  
Best Local Similarity 82.8%; Pred. No. 1e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 AATTCTGGGCTTGAAAAAGCTTGTGA 35  
DB 44328 AATTATGGGCTTGAAAAAGTTTATGA 44300

RESULT 5  
US-09-949-016-12968/c  
Sequence 12968, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12968  
LENGTH: 222452  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12968

Query Match 56.8%; Score 21; DB 3; Length 222452;  
Best Local Similarity 82.8%; Pred. No. 1.3e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGAATCTGGGCTTGAAAAAGCTTGT 32  
DB 84712 TGAATCTGGTTTGAAAAAGTCTGT 84684

RESULT 6  
US-09-257-584-5  
Sequence 5, Application US/09257584A  
Patent No. 6177611  
GENERAL INFORMATION:  
APPLICANT: Rice, Douglas A.  
TITLE OF INVENTION: Constitutive Maize Promoters  
FILE REFERENCE: 5718-33, 035718/175218  
CURRENT APPLICATION NUMBER: US/09/257,584A  
CURRENT FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 60/076,075  
EARLIER FILING DATE: 1998-02-26  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5

LENGTH: 1022  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: efla-15 promoter  
US-09-257-584-5

Query Match 56.2%; Score 20.8; DB 3; Length 1022;  
Best Local Similarity 78.1%; Pred. No. 53;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGAATCTGGGCTTGAAAAAGCTTGTGAC 36  
DB 106 GGAATATGAGCTTGAAAAAGCTTGATACAC 137

RESULT 7  
US-09-257-584-4  
Sequence 4, Application US/09257584A  
Patent No. 6177611  
GENERAL INFORMATION:  
APPLICANT: Rice, Douglas A.  
TITLE OF INVENTION: Constitutive Maize Promoters  
FILE REFERENCE: 5718-33, 035718/175218  
CURRENT APPLICATION NUMBER: US/09/257,584A  
CURRENT FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 60/076,075  
EARLIER FILING DATE: 1998-02-26  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 1023  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: efla-11 promoter  
US-09-257-584-4

Query Match 56.2%; Score 20.8; DB 3; Length 1023;  
Best Local Similarity 78.1%; Pred. No. 53;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGAATCTGGGCTTGAAAAAGCTTGTGAC 36  
DB 105 GGAATATGAGCTTGAAAAAGCTTGATACAC 136

RESULT 8  
US-09-598-401C-95/c  
Sequence 95, Application US/09598401C  
Patent No. 6596925  
GENERAL INFORMATION:  
APPLICANT: Pereira, J. Ranjan  
APPLICANT: Bagleton, Clare  
APPLICANT: Rice, Stephen J.  
TITLE OF INVENTION: Compositions and Methods for the  
Modification of Gene Expression  
FILE REFERENCE: 11000.1036c2  
CURRENT APPLICATION NUMBER: US/09/598,401C  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599  
PRIOR FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 95  
LENGTH: 2546  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-09-598-401C-95

Query Match 56.2%; Score 20.8; DB 3; Length 2546;  
Best Local Similarity 78.1%; Pred. No. 64;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GCATGAATTCGGCTTGAAAAAGCCTTGTTT 33  
DB 1189 CTTGATTCAGTCTGTGAAAAAGCCTTGCTT 1158

RESULT 9  
US-09-949-016-35388

/ Sequence 35388, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 35388

/ LENGTH: 601  
/ TYPE: DNA  
/ ORGANISM: Human

US-09-949-016-35388

Query Match 54.6%; Score 20.2; DB 3; Length 601;  
Best Local Similarity 75.8%; Pred. No. 85;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCCTTGTTT 33  
DB 273 GCATGAATTCCTGTGTTGAAAGAGCTTATAT 305

RESULT 10

US-09-949-016-35389

/ Sequence 35389, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 35389

/ LENGTH: 601  
/ TYPE: DNA  
/ ORGANISM: Human

US-09-949-016-35389

Query Match 54.6%; Score 20.2; DB 3; Length 601;  
Best Local Similarity 75.8%; Pred. No. 85;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCCTTGTTT 33  
DB 118 GCATGAATTCCTGTGTTGAAAGAGCTTATAT 150

RESULT 11

US-09-949-016-44447

/ Sequence 44447, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 44447

/ LENGTH: 601  
/ TYPE: DNA  
/ ORGANISM: Human

US-09-949-016-44447

Query Match 54.6%; Score 20.2; DB 3; Length 601;  
Best Local Similarity 75.8%; Pred. No. 85;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCCTTGTTT 33  
DB 273 GCATGAATTCCTGTGTTGAAAGAGCTTATAT 305

RESULT 12

US-09-949-016-44448

/ Sequence 44448, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
/ CURRENT APPLICATION NUMBER: US/09/949,016  
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498  
/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 44448

/ LENGTH: 601  
/ TYPE: DNA  
/ ORGANISM: Human

US-09-949-016-44448

Query Match 54.6%; Score 20.2; DB 3; Length 601;  
Best Local Similarity 75.8%; Pred. No. 85;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCCTTGTTT 33  
DB 118 GCATGAATTCCTGTGTTGAAAGAGCTTATAT 150

```
RESULT 13
; US-09-533-559-5172/c
; Sequence 5172, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849 200-us
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 1999-03-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5172
; LENGTH: 679
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; US-09-533-559-5172

Query Match      54.6%; Score 20.2; DB 3; Length 679;
Best Local Similarity 75.8%; Pred. No. 87;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      3 ATGGAATTCGGGCTTGAAAAAGCGTTGTA 35
Db      134 ATAGCATTCCTGCTTGAGAGCGGCTGTGGA 102

RESULT 14
; US-09-949-016-16039/c
; Sequence 16039, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16039
; LENGTH: 50810
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16039

Query Match      54.6%; Score 20.2; DB 3; Length 50810;
Best Local Similarity 88.0%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 ATGGAATTCGGGCTTGAAAAAGCG 27
Db      26480 AGGGAATTTGGGCTTGAGAGCGC 26456

RESULT 15
; US-09-949-016-12642
; Sequence 12642, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12642
; LENGTH: 54452
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12642

Query Match      54.6%; Score 20.2; DB 3; Length 54452;
Best Local Similarity 75.8%; Pred. No. 2.1e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 GCATGGAATTCGGGCTTGAAAAAGCGTTGTT 33
Db      43064 GCATGGAATTCCTGTGTTGAAAGAGCTTATAT 43096

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Job time : 61.3542 secs
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 04:17:10 ; Search time 637.094 Seconds

(without alignments)  
713.619 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37

Sequence: 1 gcattggaattctggccttgaagaaagcgttgcacc 37

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	37	US-09-211-691-5	Sequence 5, Appl1
2	37	100.0	37	US-10-317-773-5	Sequence 5, Appl1
3	37	100.0	37	US-10-317-773-5	Sequence 5, Appl1
4	26.4	71.4	16878	US-10-915-740A-62	Sequence 62, Appl1
5	26.4	71.4	2242716	US-10-915-740A-1068	Sequence 1068, Appl1
6	24.4	65.9	598	US-10-750-185-19677	Sequence 19677, A
7	24.4	65.9	598	US-10-750-623-19677	Sequence 19677, A
8	24.4	65.9	795	US-10-750-185-29101	Sequence 29101, A
9	24.4	65.9	795	US-10-750-623-29101	Sequence 29101, A
10	24.4	65.9	1386	US-10-437-963-88295	Sequence 88295, A
11	24.4	65.9	1752	US-10-437-963-88295	Sequence 88295, A
12	24.4	65.9	460	US-10-027-632-34789	Sequence 34789, A
13	24.2	65.4	460	US-10-027-632-34789	Sequence 34789, A
14	23.2	62.3	13	US-11-097-143-25837	Sequence 25837, A
15	22.8	61.6	1734	US-10-302-172-243	Sequence 243, Appl
16	22.8	61.6	560	US-09-925-065A-542557	Sequence 542557, A
17	22.8	61.6	560	US-09-925-065A-542557	Sequence 542557, A

18	22.8	61.6	584	US-10-437-963-88306	Sequence 88306, A
19	22.8	61.6	5848	US-10-017-161-1659	Sequence 1659, A
20	22.6	61.1	3773	US-10-108-260A-841	Sequence 841, Appl
21	21.8	58.9	369	US-09-925-065A-123503	Sequence 123503, A
22	21.8	58.9	369	US-09-925-065A-123503	Sequence 123503, A
23	21.8	58.9	377	US-10-301-480-221380	Sequence 221380, A
24	21.8	58.9	377	US-10-301-480-834789	Sequence 834789, A
25	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
26	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
27	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
28	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
29	21.8	58.9	523	US-10-301-480-118201	Sequence 118201, A
30	21.8	58.9	523	US-10-301-480-118202	Sequence 118202, A
31	21.8	58.9	523	US-10-301-480-731610	Sequence 731610, A
32	21.8	58.9	523	US-10-301-480-731611	Sequence 731611, A
33	21.8	58.9	614	US-10-301-480-250004	Sequence 250004, A
34	21.8	58.9	614	US-10-301-480-863413	Sequence 863413, A
35	21.8	58.9	621	US-09-925-065A-156805	Sequence 156805, A
36	21.8	58.9	621	US-09-925-065A-156805	Sequence 156805, A
37	21.6	58.4	854	US-10-425-115-3254	Sequence 3254, A
38	21.6	58.4	1096	US-10-425-114-17871	Sequence 17871, A
39	21.6	58.4	1180	US-10-425-114-35457	Sequence 35457, A
40	21.6	58.4	1256	US-10-425-115-39969	Sequence 39969, A
41	21.6	58.4	1277	US-10-425-115-39967	Sequence 39967, A
42	21.6	58.4	2017	US-10-450-763-16289	Sequence 16289, A
43	21.6	58.4	2165	US-10-450-763-4449	Sequence 4449, A
44	21.4	57.8	482	US-10-301-480-16119	Sequence 16119, A
45	21.4	57.8	482	US-10-301-480-629528	Sequence 629528, A

## ALIGNMENTS

RESULT 1  
US-09-211-691-5  
Sequence 5, Application US/09211691  
Patent No. US20020034805A1  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Young, N. Martin  
APPLICANT: Makarchuk, Warren W.  
APPLICANT: National Research Council of Canada  
TITLE OF INVENTION: Fusion Proteins for Use in Enzymatic Synthesis of  
FILE REFERENCE: 019957-012910US  
CURRENT APPLICATION NUMBER: US/09/211,691  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: US 60/069,443  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 37  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:SIAM-22F 5'  
OTHER INFORMATION: primer  
US-09-211-691-5  
Query Match 100.0%; Score 37; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCATGGAATTCGGCCTTGAAGAAAGCCTGTTGACC 37  
DB 1 GCATGGAATTCGGCCTTGAAGAAAGCCTGTTGACC 37  
RESULT 2  
US-10-317-773-5  
Sequence 5, Application US/10317773  
Publication No. US20030180928A1

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/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Fusion Protein Comprising a UDE-GalNac 4' Epimerase and a
/ FILE REFERENCE: 019633-000812US
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F 5'
US-10-317-773-5
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Query Match          100.0%; Score 37; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
DB      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
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RESULT 3
US-10-317-428-5
/ Sequence 5, Application US/10317428
/ Publication No. US20030186414A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ TITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
/ FILE REFERENCE: 019633-000811US
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F 5'
US-10-317-428-5
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Query Match          100.0%; Score 37; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
DB      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
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RESULT 4
US-10-915-740A-62/C
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/ Sequence 62, Application US/10915740A
/ Publication No. US20050191316A1
/ GENERAL INFORMATION:
/ APPLICANT: Frazer, Claire M.
/ APPLICANT: Hickey, Erin
/ APPLICANT: Peterson, Jeremy
/ APPLICANT: Tettelin, Hervé
/ APPLICANT: Venter, J. Craig
/ APPLICANT: Masiagnani, Vega
/ APPLICANT: Galeotti, Cesira
/ APPLICANT: Mora, Manroza
/ APPLICANT: Ratti, Giulio
/ APPLICANT: Scarselli, Maria
/ APPLICANT: Scariato, Vincenzo
/ APPLICANT: Rappuoli, Rino
/ APPLICANT: Pizzi, Mariagrazia
/ APPLICANT: Grandi, Guido
/ TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
/ FILE REFERENCE: 002441.00090
/ CURRENT FILING DATE: 2004-08-11
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR APPLICATION NUMBER: USN 60/103,794
/ PRIOR FILING DATE: 1998-10-09
/ PRIOR APPLICATION NUMBER: USN 60/132,068
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: PCT/US99/25373
/ PRIOR FILING DATE: 1999-10-08
/ NUMBER OF SEQ ID NOS: 1068
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 62
/ LENGTH: 16878
/ TYPE: DNA
/ ORGANISM: Neisseria meningitidis
US-10-915-740A-62

Query Match          71.4%; Score 26.4; DB 10; Length 16878;
Best Local Similarity 96.4%; Pred. No. 3.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      10 TCTGGCGTTGAAAAAGCGTTGTTGACC 37
DB      5806 TATGGCGTTGAAAAAGCGTTGTTGACC 5779
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RESULT 5
US-10-915-740A-1068
/ Sequence 1068, Application US/10915740A
/ Publication No. US20050191316A1
/ GENERAL INFORMATION:
/ APPLICANT: Frazer, Claire M.
/ APPLICANT: Hickey, Erin
/ APPLICANT: Peterson, Jeremy
/ APPLICANT: Tettelin, Hervé
/ APPLICANT: Venter, J. Craig
/ APPLICANT: Masiagnani, Vega
/ APPLICANT: Galeotti, Cesira
/ APPLICANT: Mora, Manroza
/ APPLICANT: Ratti, Giulio
/ APPLICANT: Scarselli, Maria
/ APPLICANT: Scariato, Vincenzo
/ APPLICANT: Rappuoli, Rino
/ APPLICANT: Pizzi, Mariagrazia
/ APPLICANT: Grandi, Guido
/ TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
/ FILE REFERENCE: 002441.00090
/ CURRENT FILING DATE: 2004-08-11
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR APPLICATION NUMBER: USN 60/103,794
/ PRIOR FILING DATE: 1998-10-09
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PRIOR APPLICATION NUMBER: USSN 60/132,068  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: PCT/US99/25373  
PRIOR FILING DATE: 1999-10-08  
NUMBER OF SEQ ID NOS: 1068  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1068  
LENGTH: 2242716  
TYPE: DNA  
ORGANISM: Neisseria meningitidis  
US-10-915-740A-1068

Query Match 71.4%; Score 26.4; DB 10; Length 2242716;  
Best Local Similarity 96.4%; Pred. No. 10;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGCCTGAAAAGCCTTTGACC 37  
DB 934750 TATGGCCTGAAAAGCCTTTGACC 934777

RESULT 6  
US-10-750-185-19677  
Sequence 19677, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19677  
LENGTH: 598  
TYPE: DNA  
ORGANISM: Bovine MMBT06634  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(69)  
OTHER INFORMATION: n is any nucleotide  
US-10-750-185-19677

Query Match 65.9%; Score 24.4; DB 10; Length 598;  
Best Local Similarity 82.4%; Pred. No. 12;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTTGAAAAGCCTTTGCA 35  
DB 81 CATGAATGCTGGGCTTGAGAAAATGCTGATTTA 114

RESULT 7  
US-10-750-623-19677  
Sequence 19677, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19677  
LENGTH: 598  
TYPE: DNA  
ORGANISM: Bovine MMBT06634  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(69)  
OTHER INFORMATION: n is any nucleotide  
US-10-750-623-19677

Query Match 65.9%; Score 24.4; DB 10; Length 598;  
Best Local Similarity 82.4%; Pred. No. 12;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTTGAAAAGCCTTTGCA 35  
DB 81 CATGAATGCTGGGCTTGAGAAAATGCTGATTTA 114

RESULT 8  
US-10-750-185-29101  
Sequence 29101, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29101  
LENGTH: 795  
TYPE: DNA  
ORGANISM: Bovine 19866880610988  
US-10-750-185-29101

Query Match 65.9%; Score 24.4; DB 10; Length 795;  
Best Local Similarity 82.4%; Pred. No. 13;  
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTTGAAAAGCCTTTGCA 35  
DB 12 CATGAATGCTGGGCTTGAGAAAATGCTGATTTA 45

RESULT 9  
US-10-750-623-29101  
Sequence 29101, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis

```
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: M11100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29101
/ LENGTH: 795
/ TYPE: DNA
/ ORGANISM: Bovine 19866880610988
US-10-437-963-29101
```

```
Query Match      65.9%; Score 24.4; DB 10; Length 795;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 CATGAATTCGGGCTTGAAAAAGGCTTTGAC 35
DB      12 CATGAATGCTGGGCTTGAGAAAAGCTTTGATT 45
```

```
RESULT 10
US-10-437-963-88295
/ Sequence 88295, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 88295
/ LENGTH: 1386
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_8715C.1
US-10-437-963-88295
```

```
Query Match      65.9%; Score 24.4; DB 8; Length 1386;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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```
QY      4 TGAATTCGGGCTTGAAAAAGGCTTTGAC 37
DB      532 TGAATGCAGGACTTGAAAAAGCTTTGCTGACC 565
```

```
RESULT 11
US-10-437-963-88327
/ Sequence 88327, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
```

```
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 88327
/ LENGTH: 1752
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_8718C.1
US-10-437-963-88327
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```
Query Match      65.9%; Score 24.4; DB 8; Length 1752;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      4 TGAATTCGGGCTTGAAAAAGGCTTTGAC 37
DB      838 TGAATGCAGGACTTGAAAAAGCTTTGCTGACC 871
```

```
RESULT 12
US-10-027-632-34789
/ Sequence 34789, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 34789
/ LENGTH: 460
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(460)
/ OTHER INFORMATION: n = A,T,C or G
US-10-027-632-34789
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```
Query Match      65.4%; Score 24.2; DB 6; Length 460;
Best Local Similarity 89.7%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 CATGAATTCGGGCTTGAAAAAGGCTTG 30
DB      44 CATGAATCCTTGCTTGAAAAAGGCTTG 72
```

```
RESULT 13
US-10-027-632-34789
/ Sequence 34789, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34789
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(460)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-34789
```

```
Query Match 65.4%; Score 24.2; DB 7; Length 460;
Best Local Similarity 89.7%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 2 CATGAAATTCGGCTTGAAAAAGCTTG 30
Db 44 CATGAAATTCCTGGCTGAGAAAAAGCTTG 72
```

```
RESULT 14
US-11-097-143-25837/C
; Sequence 25837, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25837
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```
; LENGTH: 2613
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-25837
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Query Match 62.7%; Score 23.2; DB 13; Length 2613;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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```
QY 1 GCATGAATTCGGCTTGAAAAAGCTTGTTGAC 36
Db 2436 GAATCGAATTCGAGCTTTCAAGAGCTGTTTAC 2401
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RESULT 15
US-10-302-172-243
; Sequence 243, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCB
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pc_FL_genes Version 2.0
; SEQ ID NO 243
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (208)..(1695)
US-10-302-172-243
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Query Match 62.2%; Score 23; DB 8; Length 1734;
Best Local Similarity 83.9%; Pred. No. 57;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 5 GGAATTCGGCTTGAAAAAGCTTGTTGA 35
Db 589 GAATTCCTGGGCTTTAAAGAGCTGCTTGA 619
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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 04:24:02 ; Search time 14.2604 Seconds  
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Title: US-09-211-691-5

Perfect score: 37  
Sequence: 1 gcacgaatcttggttgaaagcttgctgacc 37

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA New:\*

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5: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	56.8	699	7	US-11-217-529-5602
2	19.6	53.0	4263	7	US-11-327-900-5
3	19.4	52.4	1904	6	US-10-505-928-546
4	18.8	50.8	3243	6	US-10-528-032-8
5	18.8	50.8	3586	6	US-10-528-032-10
6	18.6	50.3	882	7	US-11-217-529-2683
7	18.6	50.3	2154	7	US-11-217-529-173201
8	18.6	50.3	2169	7	US-11-217-529-4118
9	18.6	50.3	2781	6	US-10-511-937-470
10	18.6	50.3	2868	7	US-11-217-529-2801
11	18.6	50.3	3856	6	US-10-505-928-208
12	18.2	49.2	1689	7	US-11-217-529-4580
13	18.2	49.2	2499	7	US-11-246-999-12
14	18.2	49.2	2522	7	US-11-246-999-23
15	18.2	49.2	2565	7	US-11-217-529-1739
16	18.2	49.2	12783	7	US-11-217-529-4700
17	18.2	49.2	852	7	US-11-217-529-76150
18	18.2	49.2	1371	7	US-11-217-529-76850
19	18.2	49.2	1899	7	US-11-217-529-77023
20	17.8	48.1	852	7	US-11-217-529-80613
21	17.8	48.1	1602	7	US-11-217-529-4421
22	17.8	48.1	2870	6	US-10-505-928-204
23	17.8	48.1	3780	6	US-10-511-937-2811
24	17.8	48.1	4887	7	US-11-217-529-2955
25	17.6	47.6	1176	7	US-11-217-529-5552

C 26	17.6	47.6	1410	7	US-11-217-529-2085	Sequence 2085, Ap
C 27	17.6	47.6	1896	7	US-11-217-529-78791	Sequence 78791, A
C 28	17.4	47.0	1951	7	US-11-217-529-173771	Sequence 173771, A
C 29	17.4	47.0	1233	7	US-11-217-529-1345	Sequence 1345, Ap
C 30	17.4	47.0	1545	7	US-11-217-529-80280	Sequence 80280, A
C 31	17.4	47.0	1590	7	US-11-217-529-77057	Sequence 77057, A
C 32	17.4	47.0	2484	6	US-10-488-619-2017	Sequence 2017, Ap
C 33	17.4	47.0	2484	6	US-11-217-529-5651	Sequence 5651, Ap
C 34	17.2	46.5	606	7	US-11-217-529-81626	Sequence 81626, A
C 35	17.2	46.5	1098	7	US-11-217-529-4515	Sequence 4515, Ap
C 36	17.2	46.5	1278	7	US-11-217-529-4515	Sequence 4515, Ap
C 37	17.2	46.5	1320	7	US-11-217-529-1053	Sequence 173303, Ap
C 38	17.2	46.5	2163	7	US-11-217-529-13271	Sequence 3271, Ap
C 39	17.2	46.5	3591	7	US-11-217-529-190821	Sequence 190821, Ap
C 40	17.2	46.5	4816	7	US-11-217-529-190890	Sequence 190890, Ap
C 41	17.2	46.5	5251	7	US-11-217-529-191127	Sequence 191127, Ap
C 42	17.2	46.5	5269	7	US-11-217-529-190899	Sequence 190899, Ap
C 43	17.2	46.5	5269	7	US-11-217-529-190913	Sequence 190913, Ap
C 44	17.2	46.5	5269	7	US-11-217-529-190944	Sequence 190944, Ap
C 45	17.2	46.5	5269	7	US-11-217-529-191008	Sequence 191008, Ap

#### ALIGNMENTS

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RESULT 1
US-11-217-529-5602/c
; Sequence 5602, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5602
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5602

Query Match      56.8%; Score 21; DB 7; Length 699;
Best Local Similarity 82.8%; Pred. No. 1.5;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 CATGAATCTTGCGCTGAAAAAGCTTG 30
DB      531 CATGAATCTGTATTAAGATAGCATG 503

RESULT 2
US-11-327-900-5
; Sequence 5, Application US/11327900
; Publication No. US20060099174A1
; GENERAL INFORMATION:
; APPLICANT: PHARMA PACIFIC
; APPLICANT: Merileet, Jean Francois
; APPLICANT: Dron, Michel
; APPLICANT: Tovey, Michael Gerard
; TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
; FILE REFERENCE: 46658/250044
; CURRENT APPLICATION NUMBER: US/11/327,900
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/203,311
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; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: GB 0002979.3
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002980.1
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002982.7
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002981.9
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3705)
US-11-327-900-5
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Query Match      53.0%; Score 19.6; DB 7; Length 4263;
Best Local Similarity 84.6%; Pred. No. 9.4;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GCATGAATTCGTGGCTTGAAGG 26
DB      771 GCATGAATTCGTGGCTTGAAGG 796
```

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RESULT 3
US-10-505-928-546
; Sequence 546, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 546
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-546
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```

Query Match      52.4%; Score 19.4; DB 6; Length 1904;
Best Local Similarity 70.3%; Pred. No. 9.2;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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```

QY      1 GCATGAATTCGTGGCTTGAAGGCTTTGACC 37
DB      476 GCATGATGTTGTGGCCGGAACCTGGCTTTGACC 512
```

```

RESULT 4
US-10-528-032-8
; Sequence 8, Application US/10528032
; Publication No. US20060101530A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RORS AS MODIFIERS OF THE P21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-068C-US
; CURRENT APPLICATION NUMBER: US/10/528,032
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 60/411,010
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
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```

; LENGTH: 3243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-528-032-8
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Query Match      50.8%; Score 18.8; DB 6; Length 3243;
Best Local Similarity 76.7%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```

QY      4 TGAATTCGTGGCTTGAAGGCTTTGTT 33
DB      2906 TGAATTCGTGGCTTGAAGGCTTTGTT 2935
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RESULT 5
US-10-528-032-10
; Sequence 10, Application US/10528032
; Publication No. US20060101530A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RORS AS MODIFIERS OF THE P21 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-068C-US
; CURRENT APPLICATION NUMBER: US/10/528,032
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 60/411,010
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 3586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-528-032-10
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Query Match      50.8%; Score 18.8; DB 6; Length 3586;
Best Local Similarity 76.7%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```

QY      4 TGAATTCGTGGCTTGAAGGCTTTGTT 33
DB      2941 TGAATTCGTGGCTTGAAGGCTTTGTT 2970
```

```

RESULT 6
US-11-217-529-2683
; Sequence 2683, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2683
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2683
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```

Query Match      50.3%; Score 18.6; DB 7; Length 882;
Best Local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      8 ATTCTGGCTTGAAGGCTTTGTT 32
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DB 634 ATTAGAGCTGAAAAAGCTTGT 658

## RESULT 7

US-11-217-529-173201  
; Sequence 173201, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 173201  
; LENGTH: 2154  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-173201

Query Match 50.3%; Score 18.6; DB 7; Length 2154;

Best Local Similarity 84.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAGGCTTGTGAC 36  
DB 1302 TGAGCTTGAAGGCTTGTGAC 1326

## RESULT 8

US-11-217-529-4118  
; Sequence 4118, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4118  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-4118

Query Match 50.3%; Score 18.6; DB 7; Length 2169;

Best Local Similarity 72.7%; Pred. No. 21;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 ATGAATTCGGCTTGAAGGCTTGTGA 35  
DB 863 ATGAATTCGGCTTGAAGGCTTGTGA 895

## RESULT 9

US-10-511-937-470/c  
; Sequence 470, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Mohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, Macdonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 470  
; LENGTH: 2781  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-511-937-470

Query Match 50.3%; Score 18.6; DB 6; Length 2781;

Best Local Similarity 72.7%; Pred. No. 22;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCATGGAATTCGGCTTGAAGGCTTGT 33  
DB 1498 GCTTAGAATTCGGCGACATGAAGGCGAGTTT 1466

## RESULT 10

US-11-217-529-2801/c  
; Sequence 2801, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2801  
; LENGTH: 2868  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2801

Query Match 50.3%; Score 18.6; DB 7; Length 2868;

Best Local Similarity 72.7%; Pred. No. 22;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 GGAATTCGGGCTTGAAGGCTTGTGACC 37  
DB 684 GGAATTCGTGATCTGAAGGCTCGATTTACC 652

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RESULT 11
US-10-505-928-208
; Sequence 208, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28667/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 208
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-208
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Query Match          50.3%; Score 18.6; DB 6; Length 3856;
Best Local Similarity 72.7%; Pred. No. 24;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 5 GGAATTCGGGCTTGAAGGCTTTGACC 37
DB 1694 GTAATCTGTGCTTGACAAAGGAGATTCTCC 1726
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RESULT 12
US-11-217-529-4580/c
; Sequence 4580, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4580
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4580
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Query Match          49.2%; Score 18.2; DB 7; Length 1689;
Best Local Similarity 74.2%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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```
QY 3 ATGGAATTCGGGCTTGAAGGCTTTGTTT 33
DB 690 ATCGAAATCGTCGATTGACAGGCGTTGTTT 660
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RESULT 13
US-11-246-999-12/c
; Sequence 12, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
```

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; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-246-999-12
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Query Match          49.2%; Score 18.2; DB 7; Length 2499;
Best Local Similarity 74.2%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 4 TGAATTCGGGCTTGAAGGCTTTGTTG 34
DB 2123 TGGCATTGGGGCTGGAATTAATTCCTTTTG 2093
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```
RESULT 14
US-11-246-999-23/c
; Sequence 23, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 2522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-246-999-23
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Query Match          49.2%; Score 18.2; DB 7; Length 2522;
Best Local Similarity 74.2%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 4 TGAATTCGGGCTTGAAGGCTTTGTTG 34
DB 2133 TGGCATTGGGGCTGGAATTAATTCCTTTTG 2103
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RESULT 15
US-11-217-529-1739/c
; Sequence 1739, Application US/11217529
; Publication No. US20060099612A1
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; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1739
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-1739

```

```

Query Match          49.2%; Score 18.2; DB 7; Length 2565;
Best Local Similarity 74.2%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      5 GGAATTCGGGCTGAAAAGGCTTGTGA 35
DB      1007 GTAATCTGGGGGTTTAAAAAGTGTTTTGA 977

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GenCore version 5.1.8  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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7: gb\_sts: \*  
8: gb\_sy: \*  
9: gb\_un: \*  
10: gb\_vl: \*  
11: gb\_ov: \*  
12: gb\_hcg: \*  
13: gb\_in: \*  
14: gb\_om: \*  
15: gb\_da: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.4	63.4	63	2	AR105314 Sequence
2	37.4	63.4	63	2	AR144761 Sequence
3	37.4	63.4	63	2	BD009737 Recombina
4	35.8	60.7	60	2	BD134501 Lipopolys
5	35.8	60.7	60	2	AR473909 Sequence
6	35.8	60.7	60	2	AR489132 Sequence
7	35.2	59.7	1149	2	AR393465 Sequence
8	35.2	59.7	1542	2	AR393466 Sequence
9	35.2	59.7	1569	2	AR224042 Sequence
10	35.2	59.7	1728	2	AR393467 Sequence
11	34.8	59.0	1034	8	ASGLYCOSY
12	34.8	59.0	1034	8	SYNHA13GT
13	33.8	57.3	530	8	AJ619718 Sequence
14	33.8	57.3	530	8	AJ619719 Expressio
15	33.8	57.3	530	8	AJ619720 Expressio
16	33.8	57.3	530	8	AJ619721 Expressio
17	33.8	57.3	867	2	AR139130 Sequence
18	33.8	57.3	867	2	AR139131 Sequence

C	19	33.8	57.3	918	2	AR139128 Sequence
C	20	33.8	57.3	918	2	AR139129 Sequence
C	21	33.8	57.3	1146	2	AX642595 Sequence
C	22	33.8	57.3	3604	2	AX642592 Sequence
C	23	33.6	56.9	206	2	A82175 Sequence
C	24	33.6	56.9	206	8	CVE243206 Cloning v
C	25	33.2	56.3	720	8	AJ617284 Synthetic
C	26	33.2	55.9	72	2	A83225 Sequence
C	27	33.2	55.9	72	2	A83226 Sequence
C	28	33.2	55.9	72	2	BD096923 Chemical
C	29	33.2	55.9	72	2	BD096924 Chemical
C	30	33.2	55.9	72	2	AR182950 Sequence
C	31	33.2	55.9	72	2	AR182951 Sequence
C	32	32.2	54.6	2013	2	AX472008 Sequence
C	33	31.2	52.9	88	2	AX512658 Sequence
C	34	30.4	51.5	3970	8	ASV14585 Artificial
C	35	30.4	51.5	4363	8	SCFV18290 Expression
C	36	29.2	49.5	3093	2	DD196882 ADAPTER-D
C	37	29.2	49.5	156441	12	AC122106 Rattus no
C	38	29	49.2	705	2	AX717008 Sequence
C	39	29	49.2	1806	2	AX404871 Sequence
C	40	29	49.2	1906	2	AX777477 Sequence
C	41	29	49.2	1977	2	AX404869 Sequence
C	42	28.8	48.8	888	2	CS086371 Sequence
C	43	28.8	48.8	898	2	BD096937 Mutated O
C	44	28.8	48.8	1653	2	BD206135 Polyvalen
C	45	28.8	48.8	1653	2	AX011208 Sequence

#### ALIGNMENTS

RESULT 1	AR105314	63 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR105314	Sequence 8 from patent US 6096529.			
DEFINITION	AR105314				
ACCESSION	AR105314.1	GI:12818911			
VERSION	AR105314.1	GI:12818911			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 63)				
AUTHORS	Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.				
TITLE	Recombinant .alpha.-2,3-sialyltransferases and their uses				
JOURNAL	Patent: US 6096529-A 8 01-AUG-2000;				
FEATURES	Location/Qualifiers				
source	1..63				
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	/mol_type="unassigned DNA"				

#### ORIGIN

Query Match 63.4%; Score 37.4; DB 2; Length 63;  
Best Local Similarity 87.2%; Pred. No. 0.0011;  
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTAGGTCGACTCATTAGTGTGATGCTGATGCTGATGCTGCTTC 47  
Db 1 CCTAGGTCGACTCATTAGTGTGATGCTGATGCTGATGCTGATGCTGCTTC 47

RESULT 2  
LOCUS AR144761 63 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 8 from patent US 6210933.  
ACCESSION AR144761  
VERSION AR144761.1 GI:15106628  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P. and

TITLE Moxon,E.Richard.  
JOURNAL Recombinant .alpha.-2,3-sialyltransferases and their uses  
PATENT US 6210933-A 6 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..63  
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## ORIGIN

Query Match 63.4%; Score 37.4; DB 2; Length 63;  
Best Local Similarity 87.2%; Pred. No. 0.0011;  
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
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Db 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47

## RESULT 3

BD009737

LOCUS BD009737 63 bp DNA linear PAT 31-JAN-2002  
DEFINITION Recombinant alpha-2,3-sialyltransferases and their uses.  
ACCESSION BD009737  
VERSION BD009737.1 GI:18638110  
KEYWORDS JP 2001503961-A/6.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.  
TITLE Recombinant alpha-2,3-sialyltransferases and their uses  
JOURNAL Patent: JP 2001503961-A 6 27-MAR-2001;  
NATIONAL RESEARCH COUNCIL OF CANADA  
OS unidentified  
PN JP 2001503961-A/6  
PD 27-MAR-2001  
PF 10-JUN-1997 JP 1997526320  
PR MICHEL GILBERT, WARREN W WAKARCHUK, MARTIN N YOUNG, PI MICHAEL P JENNINGS  
PC C12N15/54, C12N15/70, C12N15/79, C12N9/10, C12N5/10, C12N1/21, PC  
C12P19/26  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Key  
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FT 1..63 /organism='unidentified'.  
FT Location/Qualifiers  
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/db\_xref="taxon:32644"

FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 63.4%; Score 37.4; DB 2; Length 63;  
Best Local Similarity 87.2%; Pred. No. 0.0011;  
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
Db 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47

## RESULT 4

BD134501

LOCUS BD134501 60 bp DNA linear PAT 18-SEP-2002  
DEFINITION Lipopolysaccharide alpha-2,3 sialyltransferase of Campylobacter jejuni and its uses.  
ACCESSION BD134501  
VERSION BD134501.1 GI:23229446  
KEYWORDS JP 2002507424-A/3.  
SOURCE synthetic construct  
ORGANISM synthetic construct

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

other sequences; artificial sequences.  
1 (bases 1 to 60)  
AUTHORS Gilbert,M. and Wakarchuk,W.W.  
TITLE Lipopolysaccharide alpha-2,3 sialyltransferase of Campylobacter jejuni and its uses  
PATENT JP 2002507424-A 3 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..60  
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/db\_xref="taxon:32630"

## COMMENT

CC Description of Artificial Sequence:CU40R 3' primer FH Key  
CC Location/Qualifiers  
FT source 1..60  
FT Location/Qualifiers  
1..60 /organism='Artificial Sequence'.  
FT Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 60.7%; Score 35.8; DB 2; Length 60;  
Best Local Similarity 85.1%; Pred. No. 0.005;  
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
Db 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47

RESULT 5  
AR473909  
LOCUS AR473909 60 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 4 from patent US 6689604.  
ACCESSION AR473909  
VERSION AR473909.1 GI:42712448  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 60)  
AUTHORS Gilbert,M. and Wakarchuk,W.W.  
TITLE Lipopolysaccharide .alpha.-2,3 sialyltransferase of Campylobacter jejuni and its uses  
JOURNAL Patent: US 6689604-A 4 10-FEB-2004;  
NATIONAL RESEARCH COUNCIL OF CANADA; Ottawa;  
CAX;

FEATURES  
source Location/Qualifiers  
1..60 /organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 60.7%; Score 35.8; DB 2; Length 60;  
Best Local Similarity 85.1%; Pred. No. 0.005;  
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47  
Db 1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGGTTCAGTCTTC 47

RESULT 6  
AR489132  
LOCUS AR489132 60 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 4 from patent US 6709834.  
ACCESSION AR489132

VERSION	KEYWORDS	AR489132.1	GI:47256034
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 60)		
TITLE	Gilbert, M. and Wakarchuk, W.W.		
JOURNAL	Lipopolysaccharide. alpha.-2,3 sialyltransferase of campylobacter jejuni and its uses		
	Patent: US 6709834-A 4 23-MAR-2004;		
	National Research Council of Canada; Ottawa; CAN;		
FEATURES	Location/Qualifiers		
source	1..60		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	60.7%; Score 35.8; DB 2; Length 60;		
Best Local Similarity	85.1%; Pred. No. 0.005; 7; Indels 0; Gaps 0;		
Matches	40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
OY	1 CCTAGGTGACCTCATTAGTGGTGAATGGTGTGATGTTCCAGATCTTC 47		
Db	1 CCTAGGTGACCTCATTAGTGGTGAATGGTGTGATGTTCCAGATCTTC 47		
RESULT 7			
AR393465/c			
LOCUS	AR393465	1149 bp	DNA
DEFINITION	Sequence 3 from patent US 6617115.		
ACCESSION	AR393465		
VERSION	AR393465.1	GI:40120036	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1149)		
TITLE	Wood, K.W., Finer, J.T., Beraud, C., Mak, J. and Sakowicz, R.		
JOURNAL	Methods of screening for modulators of cell proliferation		
	Patent: US 6617115-A 3 09-SEP-2003;		
	Cytokinetics, Inc.; South San Francisco, CA		
FEATURES	Location/Qualifiers		
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	/organism="unknown"		
	/mol_type="genomic DNA"		
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Best Local Similarity	83.3%; Pred. No. 0.0053;		
Matches	40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;		
OY	12 TCATTAGTGTGATGTTGATGTTTTCAGTCTTCCTCGCTGATCAG 59		
Db	1149 TCAGTGTGTGTGTGTGTGTCTCTCATGATGATGCTCTCGCTGATCAG 1102		
RESULT 8			
AR393466/c			
LOCUS	AR393466	1542 bp	DNA
DEFINITION	Sequence 5 from patent US 6617115.		
ACCESSION	AR393466		
VERSION	AR393466.1	GI:40120038	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1542)		
TITLE	Wood, K.W., Finer, J.T., Beraud, C., Mak, J. and Sakowicz, R.		
JOURNAL	Methods of screening for modulators of cell proliferation		
	Patent: US 6617115-A 5 09-SEP-2003;		
	Cytokinetics, Inc.; South San Francisco, CA		
FEATURES	Location/Qualifiers		

ORIGIN	1..1542	/organism="unknown"	/mol_type="genomic DNA"
Query Match	59.7%;	Score 35.2;	DB 2; Length 1542;
Best Local Similarity	83.3%;	Pred. No. 0.005;	
Matches	40;	Conservative 0;	Mismatches 8; Indels 0; Gaps 0;
OY	12 TCATTAGTGTGATGTCGTGATGTCCTTCTTCGCTGATCAG	59	
DB	1542 TCACTGGTGTGTCGTGTCCTGATCAGGTCCTCCTCGCTGATCAG	1495	
RESULT 9	AR224042	1569 bp	DNA
LOCUS	Sequence 3	from patent US 6440684.	linear
DEFINITION	AR224042		PAT 26-SEP-2002
ACCESSION	AR224042		
VERSION	AR224042.1	GI:23332661	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1569)		
AUTHORS	Beraud,C., Finet,J.T., Sakowicz,R. and Wood,K.W.		
TITLE	Methods of identifying modulators of kinesin motor proteins		
JOURNAL	Patent: US 6440684-A 3 27-AUG-2002;		
FEATURES	Cytokinetics, Inc.; South San Francisco, CA		
SOURCE	1..1569		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	59.7%;	Score 35.2;	DB 2; Length 1569;
Best Local Similarity	83.3%;	Pred. No. 0.005;	
Matches	40;	Conservative 0;	Mismatches 8; Indels 0; Gaps 0;
OY	12 TCATTAGTGTGATGTCGTGATGTCCTTCTTCGCTGATCAG	59	
DB	1569 TCACTGGTGTGTCGTGTCCTGATCAGGTCCTCCTCGCTGATCAG	1522	
RESULT 10	AR393467	1728 bp	DNA
LOCUS	Sequence 7	from patent US 6617115.	linear
DEFINITION	AR393467		PAT 18-DEC-2003
ACCESSION	AR393467		
VERSION	AR393467.1	GI:40120040	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1728)		
AUTHORS	Wood,K.W., Finet,J.T., Beraud,C., Mak,J. and Sakowicz,R.		
TITLE	Methods of screening for modulators of cell proliferation		
JOURNAL	Patent: US 6617115-A 7 09-SEP-2003;		
FEATURES	Cytokinetice, Inc.; South San Francisco, CA		
SOURCE	Location/Qualifiers		
ORIGIN	1..1728		
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	/mol_type="genomic DNA"		
Query Match	59.7%;	Score 35.2;	DB 2; Length 1728;
Best Local Similarity	83.3%;	Pred. No. 0.0049;	
Matches	40;	Conservative 0;	Mismatches 8; Indels 0; Gaps 0;
OY	12 TCATTAGTGTGATGTCGTGATGTCCTTCTTCGCTGATCAG	59	
DB	1728 TCACTGGTGTGTCGTGTCCTGATCAGGTCCTCCTCGCTGATCAG	1681	



FEATURES  
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Location/Qualifiers  
1..530  
/organism="Expression vector pVT1"  
/mol\_type="other DNA"  
/db\_xref="taxon:262220"  
73..471  
/experiment="experimental evidence, no additional details recorded"

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/transl\_table=1  
/product="pentavalent protein 1 precursor"  
/protein\_id="CAF22053.1"  
/db\_xref="GI:41411188"  
/translation="MKKTATATVALAGFATVAQAVFVRSRGGSGGGSTPDCVTG  
KVEYTKYNDDEDTFVKGDEKELPTNRANLQSLLSAQITGMVTITKNACHNGGFSSE  
VIFRGGSGGLAGSEOKLISEBDLNHHHH"  
73..135  
/experiment="experimental evidence, no additional details recorded"

sig\_peptide  
/note="ompa leader"  
136..468  
/product="pentavalent protein 1 precursor"  
/experiment="experimental evidence, no additional details recorded"

mat\_peptide  
136..468  
/product="pentavalent protein 1 precursor"  
/experiment="experimental evidence, no additional details recorded"

ORIGIN  
Query Match 57.3%; Score 33.8; DB 8; Length 530;  
Best Local Similarity 84.4%; Pred. No. 0.023;  
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59  
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

RESULT 14  
AJ619719/c  
LOCUS  
DEFINITION  
AJ619719 530 bp DNA linear SYN 19-FEB-2004  
Expression vector pVT2 synthetic gene for pentavalent protein 2  
precursor.  
AJ619719.1 GI:41411189  
pentavalent protein 2.  
Expression vector pVT2  
Expression vector pVT2  
other sequences; artificial sequences; vectors.  
1  
Zhang, J. and Mackenzie, R.  
Plasmid vectors for the construction of pentavalent proteins  
unpublished  
2 (bases 1 to 530)  
Zhang, J.  
Direct Submission  
Submitted (16-DEC-2003) Zhang J., Institute for Biological  
Sciences, National Research Council, 100 Sussex Dr., Ottawa,  
Ontario, K1A 0R6, CANADA  
Location/Qualifiers  
1..530  
/organism="Expression vector pVT2"  
/mol\_type="other DNA"  
/db\_xref="taxon:262221"  
73..471  
/experiment="experimental evidence, no additional details recorded"

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/transl\_table=1  
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/protein\_id="CAF22054.1"  
/db\_xref="GI:41411190"  
/translation="MKKTATATVALAGFATVAQAVFVRSRGGSGGGSTPDCVTG  
KVEYTKYNDDEDTFVKGDEKELPTNRANLQSLLSAQITGMVTITKNACHNGGFSSE  
VIFRGGSGGLAGSEOKLISEBDLNHHHH"  
73..135  
/experiment="experimental evidence, no additional details recorded"

sig\_peptide  
/note="ompa leader"  
136..468  
/product="pentavalent protein 2 precursor"  
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source  
Location/Qualifiers  
1..530  
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/mol\_type="other DNA"  
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73..471  
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/db\_xref="GI:41411192"  
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KVEYTKYNDDEDTFVKGDEKELPTNRANLQSLLSAQITGMVTITKNACHNGGFSSE  
VIFRGGSGGLAGSEOKLISEBDLNHHHH"  
73..135  
/experiment="experimental evidence, no additional details recorded"

sig\_peptide  
/note="ompa leader"  
136..468  
/product="pentavalent protein 3 precursor"  
/experiment="experimental evidence, no additional details recorded"

mat\_peptide  
136..468  
/product="pentavalent protein 3 precursor"  
/experiment="experimental evidence, no additional details recorded"

ORIGIN  
Query Match 57.3%; Score 33.8; DB 8; Length 530;  
Best Local Similarity 84.4%; Pred. No. 0.023;  
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59  
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

RESULT 15  
AJ619720/c  
LOCUS  
DEFINITION  
AJ619720 530 bp DNA linear SYN 19-FEB-2004  
Expression vector pVT3 synthetic gene for pentavalent protein 3  
precursor.  
AJ619720.1 GI:41411191  
pentavalent protein 3.  
Expression vector pVT3  
Expression vector pVT3  
other sequences; artificial sequences; vectors.  
1  
Zhang, J. and Mackenzie, R.  
Plasmid vectors for the construction of pentavalent proteins  
unpublished  
2 (bases 1 to 530)  
Zhang, J.  
Direct Submission  
Submitted (16-DEC-2003) Zhang J., Institute for Biological  
Sciences, National Research Council, 100 Sussex Dr., Ottawa,  
Ontario, K1A 0R6, CANADA  
Location/Qualifiers  
1..530  
/organism="Expression vector pVT3"  
/mol\_type="other DNA"  
/db\_xref="taxon:262222"  
73..471  
/experiment="experimental evidence, no additional details recorded"

CDS  
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/transl\_table=1  
/product="pentavalent protein 3 precursor"  
/protein\_id="CAF22055.1"  
/db\_xref="GI:41411192"  
/translation="MKKTATATVALAGFATVAQAVFVRSRGGSGGGSTPDCVTG  
KVEYTKYNDDEDTFVKGDEKELPTNRANLQSLLSAQITGMVTITKNACHNGGFSSE  
VIFRGGSGGLAGSEOKLISEBDLNHHHH"  
73..135  
/experiment="experimental evidence, no additional details recorded"

sig\_peptide  
/note="ompa leader"  
136..468  
/product="pentavalent protein 3 precursor"  
/experiment="experimental evidence, no additional details recorded"

mat\_peptide  
136..468  
/product="pentavalent protein 3 precursor"  
/experiment="experimental evidence, no additional details recorded"

ORIGIN  
Query Match 57.3%; Score 33.8; DB 8; Length 530;  
Best Local Similarity 84.4%; Pred. No. 0.023;  
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59  
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

Fri May 19 11:37:23 2006

us-09-211-691-6.rge

Page 6

Search completed: May 19, 2006, 01:27:34  
Job time : 1259.67 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 22:50:10 ; Search time 282.094 Seconds  
(without alignments)  
1458.248 Million cell updates/sec

Title: US-09-211-691-6

Perfect score: 59  
Sequence: 1 cccagtcgacatcatcagtg.....aggctctctcgcgcgacacag 59

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	59	2	AAx84285
2	37.4	63.4	63	2	AAV04130
3	35.8	60.7	60	2	AAZ25695
4	35.2	59.7	1149	4	AAc85781
5	35.2	59.7	1542	4	AAc85782
6	35.2	59.7	1569	6	ABSS5161
7	35.2	59.7	1728	4	AAc85783
8	33.8	57.3	867	2	AAV10119
9	33.8	57.3	867	4	AAAD04539
10	33.8	57.3	867	4	AAAD04540
11	33.8	57.3	867	9	ACA62170
12	33.8	57.3	867	12	ADOS2300
13	33.8	57.3	867	12	ADOS2298
14	33.8	57.3	885	6	ABK97798
15	33.8	57.3	918	2	AAV10118
16	33.8	57.3	918	4	AAAD04537
17	33.8	57.3	918	4	AAAD04538
18	33.8	57.3	918	9	ACA62168

C	19	33.8	57.3	918	12	ADOS2295	Ados2295 Human ant
C	20	33.8	57.3	918	12	ADOS2297	Ados2297 Human ant
C	21	33.8	57.3	1152	6	ABK97808	Abk97808 DNA encod
C	22	33.8	57.3	3604	6	ABK97805	Abk97805 Interfero
C	23	33.6	56.9	206	2	AAV81221	Aav81221 Plasmid p
C	24	33	55.9	72	2	AAV72070	Aav72070 806.077 s
C	25	33	55.9	72	2	AAV72071	Aav72071 806.077 s
C	26	32.2	54.6	2013	6	ABU59152	Abu59152 Sequence
C	27	31.2	52.9	88	6	ABN84817	Abn84817 Human DNA
C	28	29.2	49.5	3093	10	ADD14876	Add14876 Phage d18
C	29	29	49.2	705	9	ADB85116	Adb85116 TNF fusio
C	30	29	49.2	1806	6	ABA99914	Ab999914 TNF-selec
C	31	29	49.2	1806	6	ABL61057	Ab161057 TNF-selec
C	32	29	49.2	1906	6	ADD13791	Add13791 Plasmid p
C	33	29	49.2	1977	6	ABA99913	Ab999913 TNF-selec
C	34	28.8	48.8	888	14	ADZ66383	Adz66383 NOFI ant
C	35	28.8	48.8	898	2	AAV73335	Aav73335 Mouse OKT
C	36	28.8	48.8	1653	3	AAZ43432	Aaz43432 Fv-antibo
C	37	28.8	48.8	1698	3	AAZ43431	Aaz43431 Fv-antibo
C	38	28.8	48.8	1794	2	AAV73337	Aav73337 Mouse bis
C	39	28.8	48.8	1817	8	ACC79606	Acc79606 Plasmid p
C	40	28.8	48.8	1817	8	ACC79607	Acc79607 Plasmid p
C	41	28.8	48.8	1897	10	ADE29201	Ade29201 Multivale
C	42	28.8	48.8	4570	4	AAE61152	Aae61152 Single ch
C	43	28.4	48.1	1574	3	AAZ57599	Aaz57599 Erythrocy
C	44	28	47.5	70	15	ABG11345	Aeg11345 P. falcip
C	45	27.4	46.4	72	2	AAZ21147	Aaz21147 C-myc pep

#### ALIGNMENTS

RESULT 1	AAx84285	AAx84285 standard; DNA; 59 BP.
ID	AAx84285	
XX		
AC	AAx84285;	
XX		
DT	08-SEP-1999	(first entry)
XX		
XX		PCR primer for alpha-2,3-sialyltransferase coding sequence.
DE		
XX		
KW	Beta-1,4-galactosyltransferase; lgtB; fusion protein; catalytic domain;	
KW	glycosyltransferase; accessory enzyme; nucleotide sugar formation;	
KW	saccharide donor; oligosaccharide synthesis; alpha-2,3-sialyltransferase;	
KW	carbohydrate structure development; PCR primer; ss.	
XX		
OS	Synthetic.	
XX		
XX	Neisseria sp.	
XX		
PN	W09991224-A2.	
XX		
PD	24-JUN-1999.	
XX		
PF	15-DEC-1998;	98WO-CA001180.
XX		
XX		
PR	15-DEC-1997;	97US-0069443P.
XX		
PR	14-DEC-1998;	98US-00211691.
XX		
PA	(CANA ) NAT RES COUNCIL CANADA.	
XX		
PI	Gilbert M, Young NM, Wakarchuk WW;	
XX		
XX	WPI; 1999-395174/33.	
DR		
XX		
XX		
PT	A new glycosyltransferase fusion protein useful in the enzymatic	
PT	synthesis of oligosaccharides.	
XX		
PS	Example 1; Page 40; 63pp; English.	
XX		
XX		
CC	This sequence represents a PCR primer for the Neisseria alpha-2,3-	
CC	sialyltransferase coding sequence. The invention relates to a nucleic	
CC	acid encoding a fusion protein that comprises a glycosyltransferase	

QY 1 CCTAGTCCACTCATTAGTGGTATGGTGGATGTTACAGTCTTCTTCGCTGATCAG 59  
1 CCTAGTCCACTCATTAGTGGTATGGTGGATGTTACAGTCTTCTTCGCTGATCAG 59

AC	AAV04130;
XX	
DT	17-JUN-1998 (first entry)
XX	

nm alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid; PCR primer;  
 KW biologically active oligosaccharide; sialyl-modified protein; ss.  
 XX

PN WO9747749-A1  
XX

PF 10-JUN-1997; 97WO-CA000390.  
XX

PR 10-JUN-1996; 96US-0019520P  
PR 07-JUN-1997; 97US-00872485  
XX

PA (CANADA) NAT RES COUNCIL CANADA.  
XX

PI Gilbert M, Wakarchuk WW, Young NM, Jennings MP;  
XXX

WPI; 1998-052313/05.

PT Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase -  
PT useful to add sialic acid to acceptor with terminal galactose residue for  
PT synthesis of biologically active oligosaccharide.  
XX

Example 2; Page 25; 50pp; English.

Av03427-01430 are PCR primers used in the amplification of novel  $\alpha$ -2,3-sialyltransferase from *Neisseria meningitidis* and *Neisseria gonorrhoeae*. The protein can be used as a reagent for adding a sialic acid residue to an acceptor having a terminal galactose residue, e.g. in the synthesis of biologically active oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid sequence can be used for the recombinant production of  $\alpha$ -2,3-sialyltransferase.

sequence 63 BP; 15 A; 9 C; 18 G; 21 T; 0 U; 0 Other;

OY	1 CCTAGGTCGACTATTAGTGGATGGTGCTGCAGGTCTTC	47
Dd	1 CCTAGGTCGACTATTAGTGGATGGTGCTGATTTTATCGTC	47

RESULT 3	
AAZ25695	
ID	AAZ25695 standard; DNA; 60 BP.
XX	

DT 05-JAN-2000 (first entry,  
XX

XX *Campylobacter jejuni* alpha-2,3-sialyltransferase PCR primer CJ40R.

campylobacter jejuni, alpha-2,3-sialyltransferase: cst-I; acceptor; lipopolysaccharide; galactose residue; sialic acid molecule; PCR primer, ss.

Synthetic.  
Campylobacter jejuni.

PN	WO9949051-A1
XX	

PD 30-SEP-1999  
VV

PF 22-MAR-1999; 99WO-CA000238.  
XX

PR	20-MAR-1998;	98US-0078891P.
PR	18-MAR-1999;	99US-00272960

(CANA ) NAT RES COUNCIL CANADA

PI Gilbert M, Wakarchuk WW;

WPI; 1999-601216/51.

New sialyltransferases useful for adding sialyl residues to acceptor molecules.

Disclosure; Page 14; 47pp; English.

Sequence 60 BP: 9 A; 17 C; 13 G; 21 T; 0 U; 0 Other;

Query Match	60.7%;	Score 35.8;	DB 2;	Length 60
Best Local Similarity	85.1%;	Pred. No. 0.031;		
Matches	40; Conservative	0; Mismatches	7; Indels	

Y  
1 CCTAGTCGACTCATTTAGTGGTATGTTGTGATGGTTTCAAGTCTTC 47  
|||||  
1 CCTAGTCGACTCATTTAGTGGTATGTTGTGATGGTTTCAAGTCTTC 47

RESULT 4  
AAC85781/c  
AAC85781 standard; cDNA; 1149 BP.

```
XX      27-OCT-1999;    99US-00428156.
PR
PA      (CYTO-) CYTOKINETICS INC.
XX
PI      Wood KW, Finer JT, Beraud C, Mak J, Sakowicz R;
XX
DR      WPI, 2001-300550/31.
P-BSDb; AAB47214.
XX
PT      Screening for drug candidates and treating cancer by using kinesin KSP.
PS      Disclosure; Fig 5; 63pp: English.
XX
CC      This sequence encodes the kinesin, KSP-K491, which may be used in the
CC      method of the invention to screen for drug candidates and bioactive
CC      agents. The method comprises combining the candidate and a cell
CC      expressing recombinant KSP, and determining the effect of the candidate
CC      on the bioactivity of recombinant KSP. Changes in the bioactivity of KSP
CC      may be determined by assays for determining changes in the mitotic
CC      spindle, particularly inhibition of mitosis, and ATP hydrolysis. It may
CC      also be determined by performing assays to determine the effect of
CC      candidate agents on apoptosis and necrosis. The method of the invention
CC      is useful for screening for drug candidates (especially bioactive agents
CC      and proteins) which effect the bioactivity of KSP, binding to KSP and/or
CC      expression of KSP, where the cells are cancer cells
SQ      Sequence 1542 BP; 528 A; 257 C; 354 G; 403 T; 0 U; 0 Other;

Query Match          59.7%; Score 35.2; DB 4; Length 1542;
Best Local Similarity 83.3%; Pred.No. 0.091;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0.

OY      12 TCATTAGTGATGATGTGGTCATGATGCATCTTTCTCGCTGATCAG 59
        |||||
Db       1542 TCAGTGTGTGTGTGTGTGTGTGTCTCATCAAGATCTCTCTCGTATCAG 1495

RESULT 6
ABS55161/C
ID ABS55161 standard; DNA; 1569 BP.
XX
AC ABS55161;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human HskIf4 construct gene.
XX
KM Microtubule stimulated Arpase; cellular proliferation; cancer; AIDS;
KW hyperplasia; resectionis; cardiac hypertrophy; immune disorder; HIV;
KW inflammation; autoimmune disease; arthritis; graft rejection; psoriasis;
KW inflammatory bowel disease; proliferation; medical procedure; surgery;
KW human immunodeficiency virus; acquired immunodeficiency syndrome;
KW angioplasty; human; HskIf4; kinesin family; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
Key Location/Qualifiers
FH   .1..1569
FT   /tag= a
FT   /product= "Human HskIf4 construct protein"
FT   misc_feature
FT           1..64
FT           /*tag= b
FT           /note= "Encodes N-terminal T7 epitope"
FT           1486..1548
FT           /*tag= c
FT           /note= "Encodes C-terminal myc epitope"
FT           1549..1566
FT           /*tag= d
FT           /note= "Encodes 6-histidine residues at C-terminus"
PN     US6440684-B1
```



PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Dan MD, Maiti PK, Kaplan HA;  
 XX  
 DR WPI; 1998-018515/02.  
 XX P-PSDB; AAM40071.  
 PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PT specific detection and treatment of neoplasia.  
 XX  
 PS Example 7; Page 94-95; 126pp; English.  
 XX  
 CC This sequence encodes a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming dimers.  
 CC This construct is used to determine the ability of H11-scFv antibody  
 CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (MAb), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma  
 CC  
 SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;  
 Query Match 57.3%; Score 33.8; DB 2; Length 867;  
 Best Local Similarity 84.4%; Pred. No. 0.24;  
 Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 15 TTAGTGTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 59  
 Db 861 TCACCTATGCTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 817  
 RESULT 9  
 AAD04539/C  
 ID AAD04539 standard; DNA; 867 BP.  
 XX  
 AC AAD04539;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human monoclonal antibody H11-single chain variable region (scFv) DNA #2.  
 XX  
 KW Human, monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..867  
 FT /tag= a  
 FT /product= "Human H11-single chain variable region (scFv)"  
 FT /transl\_except= (pos:853..864, aa:His-Lys)  
 FT /note= "Insertion of two inframe stop codon alters the  
 FT reading frame; CDS does not include start and stop  
 FT codons"  
 FT /partial  
 XX  
 XX US6207153-B1.  
 XX  
 XX 27-MAR-2001.  
 XX  
 XX 22-MAY-1997; 97US-00862124.  
 XX  
 XX 22-MAY-1996; 96US-00657449.  
 XX  
 PR 22-MAY-1996; 96US-00657449.

XX  
 PA (VIVE-) VIVENTIA BIOTECH INC.  
 XX  
 PI Dan MD, Maiti PK, Kaplan HA;  
 XX  
 DR WPI; 2001-289584/30.  
 XX P-PSDB; AAE00948.  
 PT Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 PS Example 7; Col 67-70; 56pp; English.  
 XX  
 CC The present DNA sequence encodes human monoclonal antibody (Mab), H11-  
 CC single chain variable region (scFv). The H11 light chain variable region  
 CC is linked to the heavy chain variable region through a (SGSGG)3 linker to  
 CC form dimers. The invention relates to human monoclonal antibody (Mab)  
 CC H11, H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of IGM  
 CC subclass which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NBGM1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in  
 CC vaccines and gene therapy  
 CC  
 SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;  
 Query Match 57.3%; Score 33.8; DB 4; Length 867;  
 Best Local Similarity 84.4%; Pred. No. 0.24;  
 Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 15 TTAGTGTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 59  
 Db 861 TCACCTATGCTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 817  
 RESULT 10  
 AAD04540  
 ID AAD04540 standard; DNA; 867 BP.  
 XX  
 AC AAD04540;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human H11-single chain variable region (scFv) complementary DNA #2.  
 XX  
 KW Human, monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..867  
 FT /tag= a  
 FT /product= "Human H11-single chain variable region (scFv)"  
 FT /transl\_except= (pos:853..864, aa:His-Lys)  
 FT /note= "Insertion of two inframe stop codon alters the  
 FT reading frame; CDS does not include start and stop  
 FT codons"  
 FT /partial  
 XX  
 XX US6207153-B1.  
 XX  
 XX 27-MAR-2001.  
 XX  
 XX 22-MAY-1997; 97US-00862124.  
 XX  
 XX 22-MAY-1996; 96US-00657449.  
 XX  
 XX (VIVE-) VIVENTIA BIOTECH INC.  
 XX  
 XX Dan MD, Maiti PK, Kaplan HA;  
 XX



XX	PF	29-AUG-2003;	2003US--00651453.
XX	PR	22-MAY-1996;	96US--00657449.
XX	PR	13-FEB-2001;	2001US--00782397.
XX	PA	(DANM/) DAN M D.	
XX	PA	(MAITP/) MAITI P K.	
XX	PA	(KAPL/) KAPLAN H A.	
XX	PI	Dan MD, Maici PK, Kaplan HA, Grad C;	
XX	DR	WPI; 2004-399136/37.	
XX	PT	Composition useful for treating neoplasia in patient, comprises antigen binding fragment of antibody specifically recognizing C-antigen	
XX	PT	recognized by antibody comprising H chain V region and L chain V region.	
XX	PS	Example 18; SEQ ID NO 18; 56bp; English.	
XX	CC	The invention relates to a composition comprising an antigen binding fragment of an antibody comprising H chain V region and L chain V region that specifically recognises C-antigen. The invention is useful for treating a patient with a neoplasia. The antigen binding fragment of the antibody is used as diagnostic and imaging reagents. The invention is useful for genetically altering cells in vivo, to treat various types of cancer. It is also useful in vaccine and gene therapy. The present sequence is human antibody H11 single chain V region fragment (scFv) complementary DNA.	
XX	SQ	Sequence 867 BP; 189 A; 241 C; 229 G; 208 T; 0 U; 0 Other;	
OY	Query Match	57.3%; Score 33.8; DB 12; Length 867;	
Dd	Best Local Similarity	84.4%; Pred. No. 0.24;	
	Matches	38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
		15 TTAGTGTGATGGTGATGGTTCAAGCTCTTCGCTGATCAG 59	
		7 TCACATATGATGGATGGTGCAGATCTTCTCGCTGATCAG 51	
RESULT 13			
ID	ADO52298/C		
AD	ADO52298 standard; DNA; 867 BP.		
AC	ADO52298;		
DT	29-JUL-2004 (first entry)		
DE	Human antibody H11 scFv DNA #2.		
KW	Antigen binding fragment; H chain V region; L chain V region; C-antigen; neoplasia; cancer; vaccine; gene therapy; human; single chain V region fragment; scFv; gene; ds.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	1..867	
FT		/tag= a	
FT		/product= "Human antibody H11 scFv protein"	
FT		/transl_except= (pos:853..864, aa:His-Lys)	
FT		/partial	
FT		/note= "No start and stop codon"	
PN	US2004091484-A1.		
PD	13-MAY-2004.		
PE	29-AUG-2003; 2003US--00651453.		
PR	22-MAY-1996; 96US--00657449.		

Query Match	Best Local Similarity	Score	DB	Length
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	84.4%;	Pred. No. 0.24;	DB 12;	Length 867;
15	TTACTGGATGGGATGGATGGATTCAGGCTTCCTTCGCTATCAG	59		
861	TCACCTAATGGTGGATGGATGGATTCAGATCTTCTTCCTGATCAG	817		
RESULT 14				
ID	ABK97798/C			
XX	ABK97798 standard; DNA; 885 BP.			
AC	ABK97798;			
XX				
DT	07-OCT-2002 (first entry)			
XX				
DE	C219scFv DNA sequence.			
XX				
KW	Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;			
KV	immunosuppressive; antiaerthritic; cytokine receptor; interferon; IFN;			
KW	cancer; haematological malignancy; viral infection; hepatitis; human;			
KV	multiple sclerosis; autoimmune disease; arthritis; ds; gene.			
XX				
OS	Synthetic.			
XX				
PN	WO200244197-A2.			
XX				
PD	06-JUN-2002.			
XX				
PF	30-NOV-2001; 2001WO-CA001701.			
XX				
PR	01-DEC-2000; 2000US-00727388.			
XX				
PA	(FISH/) FISH E. N.			
XX				
PI	Fish EN;			
XX				
DR	WPI; 2002-547689/58.			
DR	P-PSDB; ABG68848.			
XX				
PT	Cytokine receptor binding peptide construct, in particular interferon			
PT	receptor binding peptide construct for use as an interferon mimetic,			





GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 00:53:30 ; Search time 2369.22 Seconds

(without alignments)  
1392.544 Million cell updates/sec

Title: US-09-211-691-6

Perfect score: 59  
Sequence: 1 cccaggtcgaccatcatgctg.....aggctcttcgctgacag 59

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29.2	49.5	687	2	BT18942 1011033C0
C 2	28.6	48.5	319	2	BT18942 OR CBA000
C 3	28.4	48.1	406	13	CW656232 OC_BBA000
C 4	28.4	48.1	718	13	CL838893 OR_CBA006
C 5	28.4	48.1	746	13	CL796515 OR_CBA000
C 6	28.2	47.8	550	1	AA305848 EST177056
C 7	28.2	47.8	689	5	CP131918 UT-HF-PQ0
C 8	28.2	47.8	929	14	CNS04DT1 tetradon
C 9	28	47.5	585	11	BH742923 g67G03.9
C 10	27.8	47.1	794	11	BH586099 BGS192TR
C 11	27.8	47.1	722	3	BUS92293 P061G11.5
C 12	27.8	47.1	855	9	DN496361 P061G11.5
C 13	27.6	46.8	702	13	CW980355 KBRH004J0
C 14	27.6	46.8	923	14	CT034862 Sus scrofa
C 15	27.4	46.4	271	8	CX110631 E1050F21
C 16	27.4	46.4	432	4	CB620284 OS11Ea05G
C 17	27.4	46.4	490	1	AU035025 AU035025
C 18	27.4	46.4	529	1	AU053252 AU053252
C 19	27.4	46.4	540	4	CB653979 OSJNEC051

C 20	27.4	46.4	555	1	AU034309
C 21	27.4	46.4	556	1	AU034310
C 22	27.4	46.4	608	3	BUS23550
C 23	27.4	46.4	609	1	AU034029
C 24	27.4	46.4	652	4	CB656293
C 25	27.4	46.4	705	2	BJ404375
C 26	27.4	46.4	973	14	CNS02C51
C 27	27	45.8	226	14	DE221435
C 28	27	45.8	227	3	BUS22015
C 29	27	45.8	231	1	DE220862
C 30	27	45.8	610	8	CV901659
C 31	27	45.8	736	5	CK448583
C 32	27	45.8	838	3	BUS27457
C 33	27	45.8	896	14	CNS07DOE
C 34	26.8	45.4	106	1	AU177814
C 35	26.8	45.4	212	1	AM143603
C 36	26.8	45.4	507	8	CO296253
C 37	26.8	45.4	516	10	DV546184
C 38	26.8	45.4	527	3	BP914583
C 39	26.8	45.4	529	1	AU169441
C 40	26.8	45.4	533	9	DR197343
C 41	26.8	45.4	565	2	BJ123223
C 42	26.8	45.4	602	8	CO382038
C 43	26.8	45.4	619	13	CL720897
C 44	26.8	45.4	626	4	CB190592
C 45	26.8	45.4	653	10	DY234643

#### ALIGNMENTS

RESULT 1  
BT18942/C  
1031033C05.Y1 C. reinhardtii CC-1690, Stress II (normalized),  
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BT18942  
VERSION BT18942.1 GI:15694637  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii  
ORGANISM Chlamydomonas reinhardtii

REFERENCE 1 (bases 1 to 687)  
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,  
Lefebvre, P., McDermott, J.P., Shlager, J., Silflow, C. and Stern, D.

TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,  
Unicellular System for Analyzing Gene Function and Regulation in  
Vascular Plants. Project: 1031

JOURNAL Unpublished (2001)  
COMMENT Contact: Charles Hauser  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000

Tel: 919 613 8159  
Fax: 919 613 8177  
Email: chauuser@duke.edu.

FEATURES  
source Location/Qualifiers

1..687  
/organism="Chlamydomonas reinhardtii"  
/mol\_type="mRNA"  
/strain="CC-1690 wild type mc+ 21gr"  
/db\_xref="taxon:3055"  
/clone\_lib="C. reinhardtii CC-1690, Stress II  
(normalized), Lambda Zap II"  
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:  
XhoI; Stress condition II library, constructed by John  
Davies and Jeffrey McDermott, combines cDNAs from CC-1690  
cells grown to mid-log phase in TAP (NH4+ - containing)  
and shifted to TAP - NO3- (24hrs); H2 production  
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant  
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +  
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).



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/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):160223"
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/cell_type="T-lymphocyte"
/clone_lib="Jurkat T-cells V1"

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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
ORIGIN

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Query Match	47.8%	Score 28.2;	DB 1;	Length 550;
Best Local Similarity	80.5%;	Pred. No. 94;		
Matches 33; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

QY 19 TGGGATGGTGGTATGGTTCAGGCTCTCTCGCATCAG 59  
| | | | | | | | | | | | | | | | | | | | | |  
Db 496 TGGGACGATGATGCTGGTGAAGGCTTCTCCGATCAG 536

RESULT 7	CF131918	689 bp	linear	EST 05-AUG-2003
LOCUS	CF131918			
DEFINITION	UI-HR-PD0-aws-1-23-0-UI.r1 NIH MCC-215 Homo sapiens cDNA clone			
ACCESSION	CF131918	IMAGE:3055846 S, mRNA sequence.		
VERSION	CF131918.1	GI:33214657		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

REFERENCE	1 (bases, 1 to 689)
AUTHORS	Ronaldo, M. F., Lennon, G. and Soares, M. B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PMID	8889548
COMMENT	Contact: Soares, MB

CONTACT: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 9250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue procurement: Mary Hendrix  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/human1.html>  
Seq primer: pYX-5.

FEATURES	Location/Qualifiers
source	1. .689

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30553846"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="MDH08 (71 plaque resistant)"
/clone_lib="NH_MGC_215"
/ncbi_Organism="Vector: pYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATGAGCCCA. Tissue was provided by Mary Hendrix."

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Query March	47.8%;	Score 28.2;	DB 5;	Length 669;
Best Local Similarity	80.5%;	Pred. No. 97;		
Matches 33;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
19 TGGTATGATGTGTGATGTCAGGTCCTTCTCCGCTATAG	59			

Db

514 TGGTACGATGATGCTGGTGAAGGCTTCTTCCCTGATCAG 554

RESULT 8	
CNS04D71	
LOCUS	
DEFINITION	CNS04D71 929 bp DNA linear GSS 01-SEP-2000
	Tetradon nigriviridis genome survey sequence pUC-ori end of clone
	103c12 of library G from Tetradon nigriviridis, genomic survey
	sequence.
ACCESSION	AL286174
VERSION	AL286174.1 GI:8024620
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetradon nigriviridis

ORGANISM	REFERENCE
Tetradon nigriviridis	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontinae; Tetradon.	
AUTHORS	1
Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W. and Welschenbach, J.	
TITLE	
Estimate of human gene number provided by genome-wide analysis using Tetradon nigriviridis DNA sequence	
JOURNAL	
Nat. Genet. 25 (2), 235-238 (2000)	
PUBMED	
10835645	
REFERENCE	
2	
Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Coenrae, C.	
AUTHORS	

TITLE	JOURNAL	PUBLISHED	REFERENCE
Characterization and repeat analysis of the compact genome of the freshwater pufferfish <i>Tetraodon nigrovittatus</i>	Genome Res.	10 (7), 939-949	(2000)
10899143			
3			(bases 1 to 929)

Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Séquençage :  
BP 191 91006 Evry cedex - FRANCE E-mail : segrtel@genoscope.cns.fr  
- Web : www.genoscope.cns.fr  
This sequence is a single read, and was generated as part of a large  
scale clone-end sequencing project of the Tetrahodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetrahodon>.

FEATURES	Location/Qualifiers
source	1. .929

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/organism="Tetracodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99893"
/clone="103C12"
/clone_lib="G"
/note="Genoscope sequence ID : COBGI03B06SP1
end : PUC-Or1"

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## ORIGIN

Query Match	47.8%	Score 28.2;	DB 14;	length 929;
Best Local Similarity	80.5%;	Pred. No. 1e+02;		
Matches	33;	Conservative	0;	Mismatches 8;
				Indels 0;
				Gaps 0;

10 ACATCATAGTGGTATGGTGGTATGGTTCAGGCTCTTCTTC 50  
205 ACATCATAGTGGTATGGTGGTATGGTCTCTGGGCGCTTCGTC 245

RESULT 9  
 BH742923/c  
 LOCUS  
 DEFINITION  
 BH742923  
 585 bp DNA linear  
 G267d03.g1 BoBude01 Brassica oleracea genomic clone G267d03 5',  
 genomic survey sequence.  
 BH742923  
 BH742923.1 GI:18877537  
 GSS.  
 CCESSTION  
 ERSION  
 YWORDS

SOURCE	Brassica oleracea
ORGANISM	Brassicaceae
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS	Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Balija,V., Cummins,D.M., Katzenberger,F., King,L., Kirchoff,K., Kuit,R., Miller,B., Muller,S., Nascimeto,L., Preston,R., Santos,L., Shah,R., Zultavern,T., Dedila,N., Rabinowitz,P.D. and McCombie,W.R.
TITLE	Whole Genome Shotgun Reads from Brassica oleracea (2002b)
JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Plate: gze7 row: d column: 03 Seq primer: -21univrev Class: shotgun High quality sequence stop: 585. Location/Qualifiers
FEATURES	location/Qualifiers
SOURCE	.585 /organism="Brassica oleracea" /mol_type="genomic DNA" /db_xref="taxon:3712" /clone="gze7d03" /clone_lib="Bobuds01" /note="Vector: M13 for .x reads, pBluescript for .b and .g reads; Site_1: EcoRV; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000D3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA provided by Pablo Rabinowicz (CSHL) and shotgun library prepared in McCombie Lab."
ORIGIN	
Query Match	47.5%; Score 28; DB 11; Length 585;
Best Local Similarity	77.3%; Pred No. 1.1e-02;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
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QY	11 CTCATTAGTGATGATGTCGTGATGTCAGGTCCTTTCCGCTG 54   
RESULT 10	BH586099 794 bp DNA linear GSS 15-DEC-2001
LOCUS	BH586099/c
DEFINITION	BOGS192TF BOGS Brassica oleracea genomic clone BOGS192, genomic survey sequence.
ACCESSION	BH586099
VERSION	BH586099.1 GI:17838557
KEYWORDS	GSS.
SOURCE	Brassica oleracea
ORGANISM	Brassicaceae
REFERENCE	Brassicaceae
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
TITLE	1 (bases 1 to 794) Ayale,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
JOURNAL	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
PUBMED	15805490
COMMENT	Other GSAs: BOGS192TF Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

FEATURES	source	location/Qualifiers
ORIGIN		1..794
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		/clone_lib="BOGS"
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ORIGIN		
Query Match	47.5%; Score 28; DB 11; Length 794;	
Best Local Similarity	77.3%; Pred. No. 1.1e+02;	
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Db	497 CGCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 454	
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LOCUS	POP1G11 Populus petioles cDNA library Populus tremula cDNA 5 prime,	
DEFINITION	mRNA sequence.	
ACCESSION	BU992293	
VERSION	BU992293.1	
KEYWORDS	GI:24103358	
SOURCE	EST.	
ORGANISM	Populus tremula	
	Populus tremula	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	
	rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.	
REFERENCE	1 (bases 1 to 722)	
AUTHORS	Umeberg, P., Bhalerao, R. R., Jansson, S. and Sterky, F.	
TITLE	The poplar tree transcriptome: Analysis of expressed sequence tags	
JOURNAL	from multiple libraries	
COMMENT	Unpublished (2002)	
	Contact: BHALERAO RUPALI R.	
	Umea Plant Science Center	
	Department of Plant Physiology	
	University of Umea, 901 87 Umea, Sweden	
	Tel: +46 90 786 5279	
	Fax: +46 90 786 6676	
	Email: rupali.bhalerao@plantphys.umu.se.	
FEATURES		
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	1..722	
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Best Local Similarity	82.1%; Pred. No. 1.3e+02;	
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Db	387 CATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 349	
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LOCUS		

DEFINITION P061G11.5PR Populus petioles cDNA library Populus tremula cDNA  
 clone P061G11 5', mRNA sequence.  
 ACCESSION DN496361  
 VERSION DN496361.1 GI:60706551  
 KEYWORDS EST.  
 SOURCE Populus tremula  
 ORGANISM Populus tremula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.  
 1 (bases 1 to 855)  
 Sterky,F., Bhalerao,R.R., Umeberg,P., Segerman,B., Nilsson,P., Brunner,A.M., Charbonnel-Campa,L., Lindvall,J.U., Tandre,K., Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P., Nilsson,O., Sandberg,G., Karlsson,U., Lundberg,J., and Jansson,S.  
 A Populus EST resource for plant functional genomics  
 Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)  
 13536603  
 COMMENT Other ESTs: P061G11, P061G11.3PR  
 Contact: Bo Segerman  
 Umea Plant Science Center, Department of Plant Physiology  
 Umea University  
 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: bo.segerman@plantphys.umu.se.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone="P061G11"  
 /tissue\_type="petioles"  
 /clone\_lib="Populus petioles cDNA library"  
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 Best Local Similarity 82.1%; Pred. No. 1.4e+02;  
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 Db 385 CATAGTGTGTGTGTGTGTGTGTTGAGTCTCTCTTAG 347  
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 CM980355  
 LOCUS KBH004005R KBH, Brassica rapa HindIII BAC library Brassica rapa  
 DEFINITION subsp. pekinensis genomic clone KBH004005, genomic survey  
 sequence.  
 CM980355  
 VERSION CM980355.1 GI:56811642  
 KEYWORDS GSS.  
 SOURCE Brassica rapa subsp. pekinensis  
 ORGANISM Brassica rapa subsp. pekinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 702)  
 Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Lim,Y.P. and Park,B.S.  
 End sequence of Brassica rapa HindIII BAC library (KBH)  
 Unpublished (2004)  
 Contact: Beom-Seok Park  
 Brassica Genomics Team  
 National Institute of Agricultural Biotechnology  
 225 Seodun-Dong, Suwon, 441-707, Korea  
 Tel: +82-31-299-1670  
 Fax: +82-31-299-1672  
 Email: pbeom@da.wo.kr  
 BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone  
 KBH004005

Seq primer: M13 Reverse  
 Class: BAC ends.  
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ORIGIN  
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 Best Local Similarity 67.2%; Pred. No. 1.5e+02;  
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 CTAGTGCATCATTTAGTGTGATGTGTGATGTTCAGTCTCTTCGTCATG 59  
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 Db 82 CGAGCCGAGTTAGTATTGGTGAAGATGATGATTCAGATTCCTTCTTCATCAG 139  
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RESULT 14 923 bp DNA linear GSS 01-NOV-2005  
 CT034862  
 LOCUS Sus scrofa genomic clone CH242-1.9B6, genomic survey sequence.  
 DEFINITION CT034862  
 ACCESSION CT034862.1 GI:78630375  
 VERSION GSS.  
 KEYWORDS Sus scrofa (pig)  
 SOURCE Sus scrofa  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 1 (bases 1 to 923)  
 Humphray,S.J., Plumb,R.W. and Durham,J.L.  
 Direct Submission  
 Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished  
 This sequence was generated from the T7 end of BAC 19B6. 19B6 is part of the CHORI-242 BAC library created by P. de Jong. Further details: [http://www.sanger.ac.uk/Projects/S\\_sus/scrofa/](http://www.sanger.ac.uk/Projects/S_sus/scrofa/).  
 Location/Qualifiers  
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 QY 5 GGTGACTCATTAGTGTGATGTGTGATGTTCAGTCTT 46  
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 Db 820 GGTGTCACATGATGTGATGTGTGATGTCTGCTGTT 779  
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RESULT 15 271 bp mRNA linear EST 03-JUN-2005  
 CX110631  
 LOCUS E1050P21 A normalized whole-life-cycle cDNA library of rice Oryza  
 DEFINITION sativa (indica cultivar-group) cDNA clone E1050P21 5', mRNA



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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 01:27:44 ; Search time 94.6458 Seconds  
(without alignments)  
1166.405 Million cell updates/sec

Title: US-09-211-691-6

Perfect score: 59  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents NA:\*
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- 3: /EMC\_Celerra\_SIDS3/prodata/2/ina/5 COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/ina/6 COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/ina/6 COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/ina/7 COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/prodata/2/ina/8 COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/prodata/2/ina/9 COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.4	63.4	63	US-08-872-485-8	Sequence 8, Appli
2	37.4	63.4	63	US-09-387-942-8	Sequence 8, Appli
3	35.8	60.7	60	US-09-272-960-4	Sequence 4, Appli
4	35.8	60.7	60	US-10-058-636-4	Sequence 4, Appli
5	35.2	59.7	1149	US-09-724-519-3	Sequence 3, Appli
6	35.2	59.7	1149	US-09-592-037-3	Sequence 3, Appli
7	35.2	59.7	1149	US-09-428-1568-3	Sequence 3, Appli
8	35.2	59.7	1542	US-09-724-519-5	Sequence 5, Appli
9	35.2	59.7	1542	US-09-592-037-5	Sequence 5, Appli
10	35.2	59.7	1542	US-09-428-1568-5	Sequence 5, Appli
11	35.2	59.7	1569	US-09-592-054-3	Sequence 3, Appli
12	35.2	59.7	1728	US-09-724-519-7	Sequence 7, Appli
13	35.2	59.7	1728	US-09-592-037-7	Sequence 7, Appli
14	35.2	59.7	1728	US-09-428-1568-7	Sequence 7, Appli
15	33.8	57.3	867	US-08-862-124-16	Sequence 16, Appli
16	33.8	57.3	867	US-08-862-124-16	Sequence 16, Appli
17	33.8	57.3	918	US-08-862-124-13	Sequence 13, Appli
18	33.8	57.3	918	US-08-862-124-15	Sequence 15, Appli
19	33	55.9	72	US-09-423-439-45	Sequence 45, Appli
20	33	55.9	72	US-09-423-439-46	Sequence 46, Appli
21	27.4	46.4	72	US-09-646-028-25	Sequence 25, Appli
22	27.4	46.4	1080	US-09-646-028-39	Sequence 39, Appli
23	27.4	46.4	1086	US-09-646-028-36	Sequence 36, Appli

C 24	27.4	46.4	1113	3	US-09-646-028-38	Sequence 38, Appli
C 25	27	45.8	1079	5	US-09-145-816-4	Sequence 4, Appli
C 26	27	45.8	1079	5	US-10-352-839A-4	Sequence 4, Appli
C 27	26.8	45.4	483	3	US-09-270-767-9516	Sequence 9516, Ap
C 28	26.8	45.4	483	3	US-09-270-767-24798	Sequence 24798, A
C 29	26.8	45.4	711	3	US-09-107-532A-1515	Sequence 1515, Ap
C 30	26.6	45.1	843	3	US-09-423-439-43	Sequence 43, Appli
C 31	26.6	45.1	864	3	US-09-423-439-47	Sequence 47, Appli
C 32	26.6	45.1	1176	3	US-09-826-509-568	Sequence 568, App
C 33	26.6	45.1	1205	2	US-08-417-103-13	Sequence 13, Appli
C 34	26.6	45.1	1634	2	US-07-816-283-1	Sequence 1, Appli
C 35	26.6	45.1	1634	2	US-08-417-103-1	Sequence 1, Appli
C 36	26.6	45.1	1634	2	US-09-016-434-1302	Sequence 1302, Ap
C 37	26.4	44.7	816	3	US-08-643-704A-47	Sequence 47, Appli
C 38	26.4	44.7	1236	3	US-08-643-704A-48	Sequence 48, Appli
C 39	25.8	43.7	699	3	US-09-252-991A-5247	Sequence 5247, Ap
C 40	25.8	43.7	1674	3	US-09-252-991A-5216	Sequence 5216, Ap
C 41	25.4	43.1	1434	3	US-09-252-991A-13254	Sequence 13254, A
C 42	25.4	43.1	1545	3	US-09-252-991A-12705	Sequence 12705, A
C 43	25.4	43.1	1548	3	US-08-668-373-13	Sequence 13, Appli
C 44	25.4	43.1	2172	3	US-09-252-991A-13088	Sequence 13088, A
C 45	25.4	43.1	57280	3	US-09-949-016-11796	Sequence 11796, A

# ALIGNMENTS

RESULT 1  
US-08-872-485-8  
Sequence 8, Application US/08872485  
Patent No. 6096529  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Wakarchuk, Warren W.  
APPLICANT: Young, N. Martin  
APPLICANT: Jennings, Michael P.  
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases  
TITLE OF INVENTION: and Their Uses  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/872,485  
FILING DATE: 07-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,520  
FILING DATE: 10-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 014137-012000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:

NAME/KEY: -  
LOCATION: 1..63  
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US-08-872-485-8

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RESULT 2  
US-09-387-942-8  
Sequence 8, Application US/09387942  
Patent No. 6210933  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Makarchuk, Warren W.  
APPLICANT: Young, N. Martin  
APPLICANT: Jennings, Michael P.  
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases  
TITLE OF INVENTION: and Their Uses  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,942  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/872,485  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 014137-012000US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..63  
OTHER INFORMATION: /note= "5' primer SIALM-17R"  
US-09-387-942-8

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Best Local Similarity 87.2%; Pred. No. 0.00082;  
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGTTTCAGTCTTC 47

RESULT 3  
US-09-272-960-4  
Sequence 4, Application US/09272960  
Patent No. 6689604  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Makarchuk, Warren W.  
APPLICANT: National Research Council of Canada  
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of  
FILE REFERENCE: 014137-013210US  
CURRENT APPLICATION NUMBER: US/09/272,960  
PRIOR FILING DATE: 1999-03-18  
EARLIER APPLICATION NUMBER: US 60/078,891  
EARLIER FILING DATE: 1998-03-20  
EARLIER APPLICATION NUMBER: US 09/272,960  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:CU40R 3' primer  
US-09-272-960-4

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Best Local Similarity 85.1%; Pred. No. 0.0029;  
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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1 CCTAGTGCACCTATTAGTGTGATGGTGTGATGTTTCAGTCTTC 47

RESULT 4  
US-10-058-636-4  
Sequence 4, Application US/10058636  
Patent No. 6709834  
GENERAL INFORMATION:  
APPLICANT: Gilbert, Michel  
APPLICANT: Makarchuk, Warren W.  
TITLE OF INVENTION: National Research Council of Canada  
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of  
FILE REFERENCE: 014137-013210US  
CURRENT APPLICATION NUMBER: US/10/058,636  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: US/09/272,960  
PRIOR FILING DATE: 1999-03-18  
PRIOR APPLICATION NUMBER: US 60/078,891  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: US 09/272,960  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:CU40R 3' primer  
US-10-058-636-4

Query Match 60.7%; Score 35.8; DB 3; Length 60;  
Best Local Similarity 85.1%; Pred. No. 0.0029;  
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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US-09-724-519-3/c
; Sequence 3, Application US/09724519
; Patent No. 6414121
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/724,519
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-724-519-3

Query Match      59.7%; Score 35.2; DB 3; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGTCAGGTCCTCTTCGCTGATCAG 59
Db      1149 TCAGTGTGTGTGTGTGTGTGTGTGTGTGCTGATCAGGTCCTCTTCGCTGATCAG 1102

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; Sequence 3, Application US/09592037
; Patent No. 6437115
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-592-037-3

Query Match      59.7%; Score 35.2; DB 3; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGTCAGGTCCTCTTCGCTGATCAG 59
Db      1149 TCAGTGTGTGTGTGTGTGTGTGTGTGTGCTGATCAGGTCCTCTTCGCTGATCAG 1102
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RESULT 7
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; Sequence 3, Application US/09428156B
; Patent No. 6617115
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; FILE REFERENCE: CYTOPO33
; CURRENT APPLICATION NUMBER: US/09/428,156B
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-428-156B-3

Query Match      59.7%; Score 35.2; DB 3; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGTCAGGTCCTCTTCGCTGATCAG 59
Db      1149 TCAGTGTGTGTGTGTGTGTGTGTGTGTGCTGATCAGGTCCTCTTCGCTGATCAG 1102

RESULT 8
US-09-724-519-5/c
; Sequence 5, Application US/09724519
; Patent No. 6414121
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/724,519
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Human
US-09-724-519-5

Query Match      59.7%; Score 35.2; DB 3; Length 1542;
Best Local Similarity 83.3%; Pred. No. 0.01;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGTCAGGTCCTCTTCGCTGATCAG 59
Db      1542 TCAGTGTGTGTGTGTGTGTGTGTGTGTGCTGATCAGGTCCTCTTCGCTGATCAG 1495

RESULT 9
US-09-592-037-5/c
```



```

: TITLE OF INVENTION: proliferation states
: FILE REFERENCE: 1014A
: CURRENT APPLICATION NUMBER: US/09/592,037
: CURRENT FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: 09/428,156
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 7
: LENGTH: 1728
: TYPE: DNA
: ORGANISM: Human
US-09-592-037-7

```

Query Match	59.7%	Score 35.2;	DB 3;	Length 1728;
Best Local Similarity	83.3%	Pred. No. 0.01;		
Matches 40;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

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RESULT 14
US-09-428-156B-7/c
; Sequence 7, Application US/09428156B
; Patent No. 661715
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; TITLE OF INVENTION: proliferation states
; FILE REFERENCE: CYP0033
; CURRENT APPLICATION NUMBER: US/09/428.156B
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
; US-09-428-156B-7

```

Query Match	Similarity	Score	DB	Length
Best Local	83.3%	Pred. No. 0.01		1728
Matches	40; conservative	0; Mismatches	8; Indels	0; Gaps

  

QY	12	TCATTAGGCGCATGCTGCTGATGGTTCAGGCTCTTCTTCCTGCATCAG	59
Db	1728	TCAGGCGGCTGCTGCTGCTGCATCAGGCTCTTCTTCCTGCATCAG	1681

RESULT 15  
 US-08-862-124-16/c  
 ; Sequence 16, Application US/08862124  
 ; Patent No. 6207153  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dan, Michael D.  
 ; APPLICANT: Maltl, Pradi P.  
 ; APPLICANT: Kaplan, Howard A.  
 ; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
 ; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
 ; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
 ; TITLE OF INVENTION: DETECTION OF CANCERS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Morrison & Foerster LLP  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto

```

1 STATE: CA
2 COUNTRY: USA
3 ZIP: 94304-1018
4
5 COMPUTER READABLE FORM:
6
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent in Release #1.0, Version #1.10
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/862,124
14 FILING DATE: 22-MAY-1997
15 CLASSIFICATION: 42A
16
17 ATTORNEY/AGENT INFORMATION:
18
19 NAME: Lehnhardt, Susan K.
20 REGISTRATION NUMBER: 33,943
21 REFERENCE/DOCKET NUMBER: 31608-20001.20
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (650) 813-5600
24 TELEFAX: (650) 494-0792
25
26 TELEX: 706141
27
28 INFORMATION FOR SEQ ID NO: 16:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 867 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: join(1..855, 862..867)
38
39 US-08-862-124-16

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Query Match	57.3%;	Score 33.8;	DB 3;	Length 867;
Best Local Similarity	84.4%;	Pred. No. 0.027;		
Matches	38;	Conservative	0;	Mismatches 7; Indels 0; Gaps 0;
OY	15	TTAAGTGGATGCTGCTGATGCTTCAGGCTTCTTCGCTGATCG	59	
Db	861	TCACATAGTGGATGCTGATGCTTCAGGCTTCTTCGCTGATCG	817	

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Job time : 94.6458 secs

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/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Fusion Protein Comprising a UDP-GalNac 4' Epimerase and a
/ FILE REFERENCE: 019633-00081US
/ CURRENT APPLICATION NUMBER: US/10/317,773
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 09/211,691
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIAM-23R 3'
US-10-317-773-6
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Query Match      100.0%; Score 59; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 2,7e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTCGATCAG 59
Db      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTCGATCAG 59
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RESULT 3
US-10-317-428-6
/ Sequence 6, Application US/10317428
/ Publication No. US2003018641A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
/ FILE REFERENCE: 019633-00081US
/ CURRENT APPLICATION NUMBER: US/10/317,428
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 09/211,691
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIAM-23R 3'
US-10-317-428-6
```

```
Query Match      100.0%; Score 59; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 2,7e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTCGATCAG 59
Db      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTCGATCAG 59
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RESULT 4
US-10-058-636-4
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/ Sequence 4, Application US/10058636
/ Publication No. US20030049270A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
/ FILE REFERENCE: 014137-013210US
/ CURRENT APPLICATION NUMBER: US/10/058,636
/ CURRENT FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: US/09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: US 60/078,891
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: US 09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:C40R 3' primer
US-10-058-636-4
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Query Match      60.7%; Score 35.8; DB 6; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.023;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Oy      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTTC 47
Db      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTTC 47
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```
RESULT 5
US-10-799-016-4
/ Sequence 4, Application US/10799016
/ Publication No. US20040152165A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
/ FILE REFERENCE: 014137-013210US
/ CURRENT APPLICATION NUMBER: US/10/799,016
/ CURRENT FILING DATE: 2004-03-11
/ PRIOR APPLICATION NUMBER: US/10/058,636
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: US 60/078,891
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: US 09/272,960
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: US 09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:C40R 3' primer
US-10-799-016-4
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Query Match      60.7%; Score 35.8; DB 8; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.023;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Oy      1 CCTAGTGCAGCTCTTAGTGTGATGCGTGTGATGCGTGTTCCTTCCTTC 47
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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-651-453-18

```

Query Match	57.3%	Score 33.8	DB 8	Length 867
Best Local Similarity	84.4%	Pred No. 0.18		
Matches 38, Conservative	0	Mismatches 7	Indels 0	Gaps 0

```

QY      15  TTAGTGCATGCTGCTGATGCTTCTTCGCTGATCAG  53
          | | | | | | | | | | | | | | | | | |
Db      7  TCACTAATGCTGATGCTGATGCTTCTTCGCTGATCAG  51

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## RESULT 13

US-09-182-397-13/c  
; Sequence 13, Application US/09782397  
; Publication No. US20030021779A1  
GENERAL INFORMATION

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FOEHLER LLP  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:

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? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/782,397

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Query Match	57.3%	Score	33.8	DB	3	Length	918
Best Local Similarity	84.4%	Pred.	No.	0.18			
Matches	38	Mismatches	0	Indels	7	Gaps	0

```

Qy      15  TTAGTGTGATGGTGGTCATGCTTCAGGCTCTTCGCGTATCAG  59
          | | | | | | | | | | | | | | | | | | | |
Db      912  TCACTAATGATGATGATGATGCTCAGATCTTCGCGTATCAG  86

```

RESULT 14

US-09-182-397-15  
; Sequence 15, Application US/09782397  
; Publication No. US20030021779A1  
GENERAL INFORMATION.

```

1      TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
2      SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
3      FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
4      DETECTION OF CANCERS
5
6      NUMBER OF DRAWINGS: 22

```

NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

```

?      COMPUTER READABLE FORM:
?
?      MEDIUM TYPE: Floppy disk
?
?      COMPUTER: IBM PC compatible
?
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?
?      SOFTWARE: PatentIn Release #1.0, Version #1.30
?
?      CURRENT APPLICATION DATA:
?
?      APPLICATION NUMBER: US/09/782,397

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? FILING DATE: 13-Feb-2001  
 ? CLASSIFICATION: <Unknown>  
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 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/862,124  
 ? FILING DATE: 1997-05-22  
 ? ATTORNEY/AGENT INFORMATION: "  
 ?

NAME: Lemnaitat, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-2000.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792

QY            15 TTAGTGTGATGGTGATGGTTCAAGTCCTTCGCTGATCAG 59  
             | | | | | | | | | | | | | | | | | |  
Db            7 TCACTAATGCTGATGGTGCATTCAGATCTTCTCGCTGATCAG 51

## RESULT 15

US-10651-453-13/c  
; Sequence 13, Application US/10651453  
; Publication No. US20040091484A1  
; PUBLICATION INFORMATION.

INVENTOR: Datt, Howard K.  
 APPLICANT: Maiti, Pradip K.  
 APPLICANT: Kaplan, Howard A.  
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,  
 TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROP

Fri May 19 11:37:24 2006

us-09-211-691-6.rnpbm

**Page 6**

```

? TITLE OF INVENTION: DETECTION OF CANCERS
? FILE REFERENCE: 316082000103
? CURRENT APPLICATION NUMBER: US/10/651,453
? CURRENT FILING DATE: 2003-08-29
? PRIOR APPLICATION NUMBER: US 09/782,397
? PRIOR FILING DATE: 2001-02-13
? PRIOR APPLICATION NUMBER: US 08/862,124
? PRIOR FILING DATE: 1997-05-22
? PRIOR APPLICATION NUMBER: US 08/657,449
? PRIOR FILING DATE: 1996-05-22
? NUMBER OF SEQ ID NOS: 29
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO: 13
? LENGTH: 918
? TYPE: DNA
? ORGANISM: Homo Sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(906)
? OTHER INFORMATION:
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (913)..(918)
? OTHER INFORMATION:
?
? US-10-651-453-13

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Query Match	57.3%	Score 33.8;	DB 8;	Length 918;
Best Local Similarity	84.4%;	Pred. No. 0.18;		
Matches 38;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	15	TTA	TG	TG	TAT	GGT	GGT	GAT	GGT	GTC	AGG	CTT	CTT	CG	CT	GAT	CAG	59
Db	912	TC	AC	TAT	GGT	GGT	GGT	GAT	GGT	CAG	ATC	TTT	CTT	CG	CT	GAT	CAG	868

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Job time : 1016.91 secs

**Page 6**

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 04:24:02 ; Search time 22.7396 Seconds  
(without alignments)  
183.064 Million cell updates/sec

Title: US-09-211-691-6  
Perfect score: 59  
Sequence: 1 ccgaagtcgactcattagtcg.....aggtctcttcgcgcgacag 59

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications NA New:
- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US09\_NEW\_PUB.seq:\*
  - 2: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US06\_NEW\_PUB.seq:\*
  - 3: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US07\_NEW\_PUB.seq:\*
  - 4: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US08\_NEW\_PUB.seq:\*
  - 5: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/PCT\_NEW\_PUB.seq:\*
  - 6: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US10\_NEW\_PUB.seq:\*
  - 7: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US11\_NEW\_PUB.seq:\*
  - 8: /EMC\_Celerra\_SIDS3/prodata/2/pubnna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	39.0	1131	7	US-11-217-529-173940
2	22.8	38.6	599	6	US-10-486-619-2934
3	22.4	38.0	507	7	US-11-301-554-1922
4	22.4	38.0	569	6	US-10-486-619-1997
5	22.2	37.6	773	7	US-11-075-891-5
6	22.2	37.6	773	7	US-11-075-891-7
7	22.2	37.6	773	7	US-11-075-891-9
8	22.2	37.6	773	7	US-11-075-891-11
9	22.2	37.6	773	7	US-11-075-891-13
10	22.2	37.6	773	7	US-11-075-891-15
11	22.2	37.6	773	7	US-11-075-891-17
12	22.2	37.6	773	7	US-11-075-891-19
13	22.2	37.6	773	7	US-11-075-891-21
14	22.2	37.6	1461	7	US-11-217-529-78814
15	22.2	37.6	1902	7	US-11-217-529-76984
16	22	37.3	539	6	US-10-486-619-1907
17	22	37.3	2973	6	US-10-196-749-583
18	21.8	36.9	2145	6	US-10-505-928-72
19	21.8	36.9	2904	7	US-11-145-307A-161
20	21.6	36.6	591	7	US-11-217-529-79752
21	21.6	36.6	624	7	US-11-301-554-1914
22	21.6	36.6	636	6	US-11-301-554-1668
23	21.6	36.6	843	6	US-10-861-934-7
24	21.6	36.6	924	6	US-10-861-934-33
25	21.6	36.6	924	6	US-10-861-934-34

c	26	21.6	36.6	924	6	US-10-861-934-35	Sequence 35, Appl
c	27	21.6	36.6	1875	6	US-11-217-529-191160	Sequence 191160,
c	28	21.6	36.6	1909	6	US-10-511-937-409	Sequence 409, App
c	29	21.6	36.6	2432	6	US-10-861-934-29	Sequence 29, Appl
c	30	21.6	36.6	5502	7	US-11-301-554-785	Sequence 785, App
c	31	21.6	36.6	6353	7	US-11-301-554-784	Sequence 784, App
c	32	21.4	36.3	1713	7	US-11-217-529-7359	Sequence 2359, App
c	33	21.4	36.3	2653	6	US-10-505-928-548	Sequence 548, App
c	34	21.4	36.3	3410	6	US-10-514-738-32	Sequence 32, Appl
c	35	21.4	36.3	8448	6	US-11-145-307A-166	Sequence 166, App
c	36	21	35.6	834	6	US-10-861-934-15	Sequence 15, Appl
c	37	21	35.6	925	6	US-10-861-934-46	Sequence 46, Appl
c	38	21	35.6	1623	6	US-10-861-934-25	Sequence 25, Appl
c	39	21	35.6	1677	7	US-11-217-529-4477	Sequence 4477, Ap
c	40	20.8	35.3	969	7	US-11-249-111-47	Sequence 47, Appl
c	41	20.8	35.3	1035	7	US-11-217-529-5814	Sequence 5814, Ap
c	42	20.8	35.3	1452	1	US-09-949-925-62	Sequence 62, Appl
c	43	20.8	35.3	1560	7	US-11-217-529-1952	Sequence 1952, Ap
c	44	20.8	35.3	1941	7	US-11-217-529-190926	Sequence 190926,
c	45	20.6	34.9	1125	7	US-11-217-529-331	Sequence 331, App

# ALIGNMENTS

RESULT 1  
US-11-217-529-173940  
; Sequence 173940, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHITIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: KUDIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 173940  
; LENGTH: 1131  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-173940

Query Match 39.0%; Score 23; DB 7; Length 1131;  
Best Local Similarity 68.1%; Pred. No. 5.8;  
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 TAGTCACATCATAGTCGATGTCGTATGTTAGCTCTTCTT 49  
Db 554 TAGTCATATGCGATGTCGTGTCGTCTGATGCCGTTGATGTT 600

RESULT 2  
US-10-486-619-2934/C  
; Sequence 2934, Application US/10486619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P. C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations v  
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2934





Query Match	37.6%	Score 22.2;	DB 7;	Length 773;
Best Local Similarity	69.8%;	Pred. No. 10;		
Matches 30; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0

QY    12 TCATTAGTGGTCGATGGTGATGGTTCAAGCTCTTTCGTG 54  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db    770 TCCTTAATGATGATGATGATGATGATGATTTAATTTCCACTTTGGTG 728

```

RESULT 11
US-11-075-891-17/c
/ Sequence 17 Application US/11075891
/ Publication No. US20060088521a1
/ GENERAL INFORMATION:
/ APPLICANT: MAHADEVAN, DARUKA
/ TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANSER TREATMENT
/ FILE REFERENCE: 263922US96
/ CURRENT APPLICATION NUMBER: US/11/075,891
/ CURRENT FILING DATE: 2005-03-10
/ PRIOR APPLICATION NUMBER: US 60/557,258
/ PRIOR FILING DATE: 2004-03-27
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 17
/ LENGTH: 773
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Peptide
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)..(767)
/ OS-11-075-891-17

```

Query Match	37.6%	Score 22.2	DB 7	Length 773
Best Local Similarity	69.8%	Pred. No. 10		
Matches	30	Conservative	0	Mismatches 13
				Indels 0
				Gaps 0
12	TCATTAGGCGATGCGTGCATGCTTCCTTCGCG	54		
770	TCCTTAATGATGATGATGATGATGATTTAAATTCACATTCGCG	728		
DB				

```

RESULT 12
US-11-075-891-19/c      ; Sequence 19, Application US/11075891
                             ; Publication No. US2006008521A1
GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 2639220S96
CURRENT APPLICATION NUMBER: US/11/075,891
PRIORITY FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19
LENGTH: 773
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: CDS
LOCATION: (3) ..(767)
US-11-075-891-19

```

Query Match	37.6%;	Score 22.2;	DB 7;	Length 773;
Best Local Similarity	69.8%;	Pred. No. 10;		
Matches	30; Conservative	0; Mismatches	13; Indels	0; Gaps

QY 12 TCATTAGTGGTGATGTTGTGATGGTTACGCTTCCTTCGCTG 54  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 770 TCCTTAATCATGATGATGATGATGTTAAATTTCCACTTTGGTG 728

```

RESULT 13
US-11-075-891-21/c
; Sequence 21. Application US/11075891
; Publication No. US2006008851A1
GENERAL INFORMATION:
APPLICANT: MAHADEVAN, DARUKA
TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
FILE REFERENCE: 2633220S96
CURRENT APPLICATION NUMBER: US/11/075,891
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: US 60/557,258
PRIOR FILING DATE: 2004-03-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 773
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: CDS
LOCATION: (3) .. (767)
US-11-075-891-21

```

	Best Match	Score 22.2;	DB 7;	Length 773;
	Query Similarity	69.8%;	Pred. No. 10;	
Matches	30; Conservative	0; Mismatches	13; Indels	0; Gaps
QY	12 TCATAGCGGAGCGGCGGACGGCTCTTTCGC	GCG 54		
Dd	770 TCCCTAATGATGATGATCATGTTTAACTTCCACTTGCG	G 728		

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RESULT 14
US-11-217-529-78814/c
? Sequence 78814, Application US/11217529
? Publication No. US20060099612A1
? GENERAL INFORMATION:
? APPLICANT: SUNTORY LIMITED
? APPLICANT: NAKAO, YOSHIIRO
? APPLICANT: NAKAMURA, NORIHISA
? APPLICANT: KODAMA, YUKIKO
? APPLICANT: FUJIMURA, TOMOKO
? APPLICANT: ASHIKARI, TOSHIIKO
? TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
? FILE REFERENCE: S-38-285
? CURRENT APPLICATION NUMBER: US/11/217,529
? CURRENT FILING DATE: 2005-09-02
? PRIOR APPLICATION NUMBER: US 10/932,182
? PRIOR FILING DATE: 2004-09-02
? NUMBER OF SEQ ID NOS: 197023
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 78814
? LENGTH: 1461
? TYPE: DNA
? ORGANISM: Saccharomyces pastorianus
US-11-217-529-78814

Query Match          37.6%; Score 22.2; DB 7; Length 1461;
Best Local Similarity 64.7%; Pred. No. 12;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0

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